

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2001, 16:20:13 ; Search time 7577.75 Seconds
(without alignments)
11971.674 Million cell updates/sec

Title: US-09-698-903B-1
Perfect score: 5865
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues
Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	4903.2	83.6		4946	9	AR098307	AR098307 Sequence 1
4	2386.8	40.7		5560	9	A60112	A60112 Sequence 5
5	2386.8	40.7		5560	9	AR098311	AR098311 Sequence
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8	1732.4	29.5		2821	13	ATRCSCA	X13611 Arabidops1s

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RESULT 2

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 VERSION A76915.1 GI:6088712
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 SOURCE Transformation vector pTHW107.
 ORGANISM Transformation vector pTHW107.
 REFERENCE 1 (bases 1 to 4946)
 AUTHORS De, B.M.
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 PLANT GENETIC SYSTEMS NV (BE)
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 BASE COUNT 1569 a 891 c 963 g 1523 t
 ORIGIN

Query Match 83.6%; Score 4903.2; DB 9; Length 4946;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 4916; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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AUTHORS	De,B.M.		
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 DB 2387 CATGCCAACCTCATGTTTGTAGTGTAATCTTTGATTTTGTCAAAATATATGTTGCTGTG 2446
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 DB 2447 ATATTGTATAAGAATTTCTTGACCATATACACACACATATATATATATATATAT 2506
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 QY 2416 taacaaccatatgttcgattgtatctcgaataactgcagagtaagtgaataataata 2475
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 QY 2476 atctattgctgaaattatctcagattgtaagattttcttaagtaaaattctttcacaattt 2535
 DB 2627 ATCTATTGCTGAAATTTATCTCAGATGTTTAAAGATTTCCTTAAAGTAAATCTTCAATTT 2686
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QY 2596 acataataaatttgaatt 2613
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 RESULT 6
 AC007152 90387 bp DNA PLN 09-AUG-2000
 LOCUS Arabidopsis thaliana chromosome I BAC F1019 genomic sequence,
 DEFINITION complete sequence.
 AC007152
 VERSION AC007152.9 GI:9581921
 KEYWORDS HTG.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 90387)
 REFERENCE
 AUTHORS Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
 Altafi,H., Nguyen,M., Lam,B., Southwick,A., Miranda,M., Brooks,S.,
 Buehler,E., Chao,Q., Chin,C., Chioi,J., Choi,E., Gonzalez,A.,
 Howng,B., Johnson-Hopson,C., Khan,S., Kim,C., Koo,T., Lee,J.M.,
 Lenz,C., Liu,A., Liu,S., Mukharsky,N., Pham,P., Sakano,H.,
 Shinn,P., Toriumi,M., Vaysberg,M., Yu,G., Ecker,J., Theologis,A.
 and Davis,R.W.
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 90387)
 AUTHORS Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
 Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P.,
 Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S.,
 Luross,S., Schwartz,J., Shinn,P., Toriumi,M., Vytokala,V.,
 Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
 TITLE Direct Submission
 JOURNAL Submitted (24-MAR-1999) DNA Sequencing and Technology Center,
 Stanford University, 855 California Avenue, Palo Alto, CA 94304,
 USA
 3 (bases 1 to 90387)
 REFERENCE
 AUTHORS Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
 Altafi,H., Nguyen,M., Lam,B., Southwick,A., Bel,Q., Buehler,E.,
 Chin,C., Chioi,J., Choi,E., Dunn,P., Gonzalez,A., Howng,B., Kim,C.,
 Koo,T., Lee,J.M., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S.,
 Mukharsky,N., Pham,P., Sakano,H., Schwartz,J., Shinn,P.,
 Thaveri,A., Toriumi,M., Vaysberg,M., Walker,M., Yu,G., Ecker,J.,
 Theologis,A. and Davis,R.W.
 TITLE Direct Submission
 JOURNAL Submitted (29-JUL-2000) DNA Sequencing and Technology Center,
 Stanford University, 855 California Avenue, Palo Alto, CA 94304,
 USA
 4 (bases 1 to 90387)
 REFERENCE
 AUTHORS Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
 Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A.
 and Davis,R.W.
 TITLE Direct Submission
 JOURNAL Submitted (09-AUG-2000) DNA Sequencing and Technology Center,
 Stanford University, 855 California Avenue, Palo Alto, CA 94304,
 USA
 COMMENT On Jul 29, 2000 this sequence version replaced gi:9186839.
 Bases 76,114-90,387 of clone F1019 overlap with bases 1-14,276 of
 'IGF' BAC clone F5A8, gb|AC004146.
 e-mail for correspondence: arab@sequence.stanford.edu
 Genes with similarity to proteins in the databases are described as
 'putative', '-like' or 'similar to'. Genes that have EST
 similarity but no significant protein similarity are described as
 'unknown proteins'. Genes that are annotated based only on gene
 prediction software are described as 'hypothetical proteins'.
 The software programs used to predict genes include: 'Grail'
 (Informatics Group, Oak Ridge National Laboratory,
 http://combio.ornl.gov/section/index.html), GENSCAN (Chris Burge,
 http://genome.stanford.edu/~chris/GENSCAN.html), Fexa (V.Solovyev
 & A.Salamov, Sanger Centre, http://genome.sanger.ac.uk/), and
 NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of
 Denmark, http://www.cbs.dtu.dk/NetPlantGene.html).

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RESULT 7

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LOCUS Arabidopsis thaliana chromosome I BAC F5A8 genomic sequence,
DEFINITION complete sequence.
AC004146
AC004146.1 GI:3540210
VERSION HTG.
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SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
1 (bases 1 to 101933)
Fedorispiet, N.A., Palm, C.J., Conway, A.B., Kurtz, D.B., Conway, A.R.,
Au, M., Araujo, R., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y.,
Oji, O., Osborne, B.I., Shinn, P., Sun, H., Toriumi, M.,
Vyotskaia, V., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
Unpublished
JOURNAL
2 (bases 1 to 101933)
Fedorispiet, N.A., Palm, C.J., Conway, A.B., Kurtz, D.B., Conway, A.R.,
Au, M., Araujo, R., Brendel, V., Buehler, E., Dewar, K., Feng, J.,
Kim, C., Li, Y., Oji, O., Osborne, B.I., Shinn, P., Sun, H., Toriumi, M.,
Vyotskaia, V., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
Direct Submission
TITLE
JOURNAL
Submitted (31-JUL-1997) Biochemistry, Stanford University/DNA
Sequencing and Technology Center, 855 California Avenue, Palo Alto,
CA 94304, USA
REFERENCE
3 (bases 1 to 101933)
Fedorispiet, N.A., Palm, C.J., Conway, A.B., Kurtz, D.B., Conway, A.R.,
Au, M., Araujo, R., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y.,
Oji, O., Osborne, B.I., Shinn, P., Sun, H., Toriumi, M., Vyotskaia, V.,

Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
Direct Submission
Submitted (04-Sep-1998) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA

4 (bases 1 to 101933)

Federspiel,N.A., Palm,C.J., Conway,A.B., Kurtz,D.B., Conway,A.R.,
Au,M., Araujo,R., Buehler,E., Dewar,K., Feng,J., Kim,C., Li,Y.,
Oji,O., Osborne,B.I., Shinn,P., Sun,H., Toriumi,M., Vyotskaia,V.,
Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
Direct Submission
Submitted (30-JAN-1999) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA

On Sep 4, 1998 this sequence version replaced gi:2934888.
Bases 90722-101933 of clone F5A8 overlap with bases 114738-103537
of 'IGF' BAC clone F1M21.

Location/Qualifiers

source

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/clone="IGF' F5A8"

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complement(15428..18947)

/gene="F5A8.3"

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/note="putative Cytochrome P450 protein; Similar to
Catharanthus roseus Cytochrome P450 gi|404690 and others.
Contains Cytochrome P450 motif"

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KDSVEIGRSSYGGDLLGLLNNQMSNNLNVMQIMDECKTFFFTGHETYSLLLTWT
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/gene="F5A8.4"

/note="Hypothetical protein; Similar to Saccharomyces
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gene

TITLE
JOURNAL

REFERENCE
AUTHORS

TITLE
JOURNAL

COMMENT

FEATURES
source

gene

CDS

gene

CDS

gene

CDS

Db 814 ACAGATTGTTACATGAAACAAAAGTCTCTGTAGATGCGCAAGATATCACAAATT 755

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Qy 4681 ataataaagaataataccaaataagctccaccccttaacttaaaataaaataaaccagc 4740

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Qy 4801 ataattctatgtatggttagaataaagaataaataatagccggtatttggtagaa 4860

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Qy 4861 aatccctataataatcg 4877

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RESULT 11

NTA29/c

LOCUS NTA29 6254 bp DNA PLN 09-MAY-1995

DEFINITION Tobacco anther-specific gene TA-29 and stem-specific gene TSJT1.

ACCESSION X52283

VERSION X52283.1

KEYWORDS GI:20035

SOURCE tissue specific gene.

ORGANISM common tobacco.

EuKaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 6254)

REFERENCE

AUTHORS Mariani, T.

TITLE Direct Submission

JOURNAL Submitted (23-MAR-1990) Mariani T., Plant Genetic Systems, J Plateaustraat 22, B 9000 Gent, Belgium

REFERENCE 2 (bases 1 to 6254)

AUTHORS Seurinck, J., Truettner, J. and Goldberg, R. B.

TITLE The nucleotide sequence of an anther-specific gene

JOURNAL Nucleic Acids Res. 18 (11), 3403 (1990)

MEDLINE 90287727

COMMENT Data kindly reviewed (13-DEC-1990) by Mariani C.

FEATURES

Location/Qualifiers

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/cultivar="Samsun"

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/clone_lib="lambda Charon32"

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DEFINITION Sequence 3 from patent US 5977433.
ACCESSION AR084079
VERSION AR084079.1 GI:10010850
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5620)
AUTHORS Williams,M. and Leemans,J.
TITLE Maintenance of male-sterile plants
JOURNAL Patent: US 5977433-A 3 02-NOV-1999;
FEATURES Location/Qualifiers
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Best Local Similarity 98.9%; Pred.No. 6.1e-179;
Matches 1291; Conservative 0; Mismatches 11; Indels 4; Gaps 1;
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DEFINITION Sequence 9 from patent US 5639948.
ACCESSION I47737
VERSION I47737.1 GI:2471702
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1. (bases 1 to 5620)
AUTHORS Michiels,F., Morioke,S., Scheirlinck,T. and Komari,T.
TITLE Stamen-specific promoters from rice
JOURNAL Patent: US 5639948-A 9 17-JUN-1997;
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Location/Qualifiers
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Search completed: November 15, 2001, 20:39:18
Job time: 15545 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2001, 16:23:38 ; Search time 328.78 Seconds
(without alignments)
11200.934 Million cell updates/sec

Title: US-09-698-903B-1

Perfect score: 5865

Sequence: 1 aattacaacggtatatcc.....caattgaatatctctgcg 5865

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	5849.8	99.7	5864	17 AAT39339	Plasmid pTColl13 T-
2	4903.2	83.6	4946	18 AAT59531	T-DNA of plasmid p
3	1500.2	25.6	3265	10 AAN92188	Ta29 gene insert i
4	1268.8	21.6	5620	13 AAQ27489	pVE108. Synthetic
5	1267.2	21.6	5620	15 AAQ53875	Plasmid pVE108 use
6	885.8	15.1	5349	19 AAV23239	T-DNA of pTTS24.
7	832.8	14.2	6539	21 AAZ91097	E. coli plasmid pT
8	832.8	14.2	6548	17 AAT39336	Plasmid pTTS174 use
9	832.8	14.2	6548	18 AAT61394	Plasmid pTTS172. C
10	832.8	14.2	6548	21 AAZ91096	E. coli plasmid pT
11	802.2	13.7	7599	22 AAT25320	Nucleotide sequenc

12	741.8	12.6	3658	17 AAT39338	Plasmid pVE136 (Ec
13	727.8	12.4	4808	15 AAQ53889	Restriction fragme
14	712	12.1	4896	17 AAT08976	pTS256 contg. p35S
15	708.8	12.1	4896	20 AAX15631	Nucleotide sequenc
16	706.8	12.1	6555	15 AAQ53874	Plasmid pVE144 use
17	705.4	12.0	6376	13 AAQ27951	pVE149. Escherich
18	595.2	10.1	1303	17 AAQ29337	Plasmid pTS88 (Eco
19	564	9.6	790	17 AAT13117	Inserted DNA fragm
20	564	9.6	790	21 AAZ39903	DNA fragment from
21	561.6	9.6	2345	19 AAV54016	Nucleotide sequenc
22	561.6	9.6	2345	20 AAX08450	T-DNA sequence of
23	561.6	9.6	2345	22 AAC58664	Agrobacterium tume
24	561.6	9.6	3544	17 AAT17246	pTS200 contg. p35S
25	561.6	9.6	3544	20 AAX15632	Nucleotide sequenc
26	561.6	9.6	3658	17 AAT39338	Plasmid pVE136 (Ec
27	561.6	9.6	4808	15 AAQ53889	Restriction fragme
28	561.6	9.6	4883	13 AAQ25709	pDE110. Synthetic
29	561.6	9.6	4883	14 AAQ51192	pDE110; plasmid DN
30	561.6	9.6	4896	17 AAT08976	pTS256 contg. p35S
31	561.6	9.6	4896	20 AAX15631	Nucleotide sequenc
32	561.6	9.6	5611	19 AAV23242	Plasmid pLH48. Sy
33	561.6	9.6	5620	13 AAQ27489	pVE108. Synthetic
34	560	9.5	6376	13 AAQ27951	pVE149. Escherich
35	558.4	9.5	5620	15 AAQ53875	Plasmid pVE108 use
36	551.8	9.4	9335	20 AAV61374	Plasmid pGFP/367 c
37	549.6	9.4	610	21 AAZ61377	Nucleotide sequenc
38	549.6	9.4	838	8 AAN71305	Sequence encoding
39	549	9.4	549	13 AAQ23354	Male organ-specifi
40	549	9.4	5611	19 AAV23242	Plasmid pLH48. Sy
41	548.8	9.4	552	18 AAT61880	Streptomyces hygro
42	491.4	8.4	6548	17 AAT39336	Plasmid pTTS174 use
43	491.4	8.4	6548	18 AAT61394	Plasmid pTTS172. C
44	491.4	8.4	6548	21 AAZ91096	E. coli plasmid pT
45	487.2	8.3	6539	21 AAZ91097	E. coli plasmid pT

ALIGNMENTS

RESULT 1
AAT39339
ID AAT39339 standard; DNA; 5864 BP.
XX
AC AAT39339;
XX
DT 22-JAN-1997 (first entry)
XX
DE Plasmid pTColl13 T-DNA used to obtain male sterile oilseed rape.
XX
KW Plasmid pTColl13; male sterile; barnase; ribonuclease; barstar;
transgenic plant; oilseed rape; canole; Brassica napus; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature complement (1..25)
FT /*tag= a
FT /label= RB
FT /note= "right border of Agrobacterium T-DNA"
FT polyA_signal complement (98..330)
FT /*tag= b
FT /label= 3'g7
FT /note= "region containing polyA signal of gene 7
of Agrobacterium T-DNA"
FT CDS complement (331..882)
FT /*tag= c
FT /label= bar
FT /note= "region coding for phosphinothricin
acetyltransferase"
FT promoter complement (883..2608)
FT /*tag= d
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FT /note= "promoter of Arabidopsis Rubisco small

FT			subunit gene"
FT	polyA_signal	complement (2659..3031)	
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FT		/label= 3'nos	
FT		/note= "region containing polyA signal of nopaline	
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FT		Nicotiana tabacum"	
FT	promoter	4924..5216	
FT		/*tag= h	
FT		/label= Pnos	
FT		/note= "promoter of nopaline synthase gene of	
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FT		/note= "region coding for barstar of Bacillus	
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XX			
PN	W09636283-A1.		
XX			
PD	29-AUG-1996.		
XX			
XX	21-FEB-1996;	96WO-EP00722.	
PX			
PR	21-FEB-1995;	95PE-0400364.	
XX			(PLBZ) PLANT GENETIC SYSTEMS NV.
PA	Botterman J,	Cornelissen M, Michiels F;	
PX			
PI	WPI; 1996-402373/40.		
DR			
XX			
PX			
PT	Prodn. of male sterile plants by transforming with a chimeric		
PT	construct - comprising a male sterility DNA e.g. barnase and a		
PT	co-regulating gene, e.g. barstar, into the nuclear genome, useful		
PT	for generating hybrid cultivars		
XX			
PS	Example 3; Page 33-3743-47; 56pp; English.		
CC			
CC	Plasmid pTColl13 (AA739339) is a T-DNA vector containing a bar gene		
CC	under control of the PSU promoter, a barnase gene under control		
CC	of the stamen-specific pTA29 promoter, and a barstar (co-regulatory)		
CC	gene under control of the Pnos promoter, 87% Of oilseed rape		
CC	plants regenerated after Agrobacterium-mediated transformation		
CC	using pTColl13 were male sterile. Barnase expression disturbed the		
CC	function of stamen cells leading to male sterility. Constitutive		
CC	expression of barstar counteracted any low level expression of		
CC	barnase in non-stamen tissue.		
XX			
SQ	Sequence 5864 BP; 1849 A; 1094 C; 1150 G; 1771 T; 0 Other;		
	Query Match	99.78; Score 5849.8; DB 17; Length 5864;	
	Best Local Similarity	99.94; Prod. No. 0;	
	Maches 5862; Conservative	0; Mismatches 2; Indels 1; Gaps	

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QY	61	gtcgtataagaagaagcaatttgtagatgttaattccattccattgtgaaagaaatactg	120
Db	61	gtcgtataagaagaagcaatttgtagatgttaattccattccattgtgaaagaaatactg	120
QY	121	atatattattgataaaatacaacagtcaggtattatagtcacagcaaaaacataattatt	180
Db	121	atatattattgataaaatacaacagtcaggtattatagtcacagcaaaaacataattatt	180
QY	181	gatgcaagttaaattcagaataatttcaataaactgattatcagctggtacattgcg	240
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QY	241	tagatgaagaactgagtgccgattattgttaatacaataaattgatgatagctagctt	300
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QY	481	gcacgctcggggtcgtttgggcagcccgcattgacagcgaccacgctctcttgaaagccctgtgcct	540
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QY	541	ccagggaacttcagcaggtgggttagagcgtggagcccagtcocgtccgctggtgcgcgg	600
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Query Match	99.7%	Score 5849.8;	DB 17;	Length 5864;
Best Local Similarity	99.9%	Pred. NO. 0;		
Matches 5862; Conservative	0;	Mismatches	2;	Indels 1; Gaps 1;

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 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 5640 atataacagttattgaataattctgaatttaaaactgcatcaataaattattgttttt 5699
 Qy 5701 gcttgactataacacatcacatcaaaattgcttttcttcttcatacgaccatgtacatcgactct 5820
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 5700 gcttgactataacacatcacatcaaaattgcttttcttcttcatacgaccatgtacatcgactct 5819
 Qy 5821 cccagatctgcagtgaggccatttacaattgaatatatctctgccc 5865
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 5820 cccagatctgcagtgaggccatttacaattgaatatatctctgccc 5864

RESULT 2

AAT59531

ID AAT59531 standard; DNA; 4946 BP.

XX AC

XX AC AAT59531;

XX DT Q7-MAY-1997 (first entry)

XX DE T-DNA of plasmid pTHW107.

XX KW

KW Transgenic plant; poly-(ADP-ribose) polymerase inhibitor; PARP;

KW niacinamide; Agrobacterium; T-DNA; male sterile; barnase;

KW ribonuclease; RNase; cereal; wheat; oilseed rape; Brassica napus;

KW plasmid pTHW107; ds.

XX OS

OS Chimeric Agrobacterium sp.;

OS Chimeric Arabidopsis thaliana;

XX OS Chimeric Nicotiana tabacum.

XX PH

XX Key Location/Qualifiers

FT misc_RNA complement (1..25)

FT FT /*tag= a

FT FT /label= RB

FT FT /note= "T-DNA right border"

FT FT complement (97..330)

FT FT /*tag= b

FT FT /label= 3'g7

FT FT /note= "3' untranslated region contg. the poly-A

FT FT signal of gene-7 of Agrobacterium T-DNA"

FT FT complement (331..882)

FT FT /*tag= c

FT FT /label= Bar

FT FT /product= phosphinothricin acetyltransferase

FT FT complement (883..2608)

FT FT /*tag= d

FT FT /label= PSSU

FT FT /note= "promoter region of Rubisco small subunit

FT FT gene of Arabidopsis thaliana"

FT FT complement (2658..3031)

FT FT /*tag= e

FT FT /label= 3'nos

FT FT /note= "3' untranslated region contg. the poly-A

FT FT signal of the nopaline-synthase gene of

FT FT Agrobacterium T-DNA"

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT CDS complement (3032..3367)
 FT FT /*tag= f
 FT FT /label= Barnase
 FT FT /product= barnase
 FT FT complement (3368..4876)
 FT FT /*tag= g
 FT FT /label= PTA29
 FT FT /note= "promoter region of tobacco TA29 gene"
 FT FT misc_RNA complement (4822..4946)
 FT FT /*tag= h
 FT FT /label= LB
 FT FT /note= "T-DNA left border"

XX EP757102-A1.

PN XX

XX 05-FEB-1997.

XX XX

XX 04-AUG-1995; 95EP-0401844.

PF XX

XX 04-AUG-1995; 95EP-0401844.

PR XX

XX (PLBZ) PLANT GENETIC SYSTEMS NV.

PA XX

XX De Block M;

PI XX

XX WPT; 1997-111050/11.

DR XX

XX Prodn. of transgenic plants using a poly-(ADP-ribose) polymerase

PT inhibitor - reduces the cultured cells response to stress and

PT reduces metabolism

PT XX

XX Example 3; Page 13-16; 25pp; English.

PS XX

XX Plasmid pTHW107 is a vector carrying T-DNA (AAT59531) comprising a

CC barnase coding sequence under control of the tobacco TA29 gene

CC stamen-specific promoter and a phosphinothricin acetyltransferase

CC coding sequence under control of an Arabidopsis Rubisco small

CC subunit gene promoter. Oilseed rape hypocotyl explants were

CC infected with Agrobacterium tumefaciens C58clrif carrying vector

CC pTHW107 and helper Ti plasmid pMP60. In some treatments, the

CC hypocotyls were treated with the poly-(ADP-ribose) polymerase

CC inhibitor niacinamide (250 mg/l) 4 days prior to infection.

CC Plants regenerated from niacinamide-treated transformed calli

CC had a low copy number and displayed less variation in the

CC expression profile of the transgenes.

XX XX

SQ Sequence 4946 BP; 1569 A; 891 C; 963 G; 1523 T; 0 other;

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Query Match 83.6%; Score 4903.2; DB 18; Length 4946;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 4916; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 aattacaacggtatatactctgccagtagctcggcgccgctggaactcggcgctgagtagcatg 60
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1 aattacaacggtatatactctgccagtagctcggcgccgctggaactcggcgctgagtagcatg 60
 Qy 61 gtcgataaagaaagcaatttgtagatgttaattcccatcttgaagaataatagtttaa 120
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 61 gtcgataaagaaagcaatttgtagatgttaattcccatcttgaagaataatagtttaa 120
 Qy 121 atattattgataaaataacaagtcaggtattattagtcgaacgaacaaataattttt 180
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 121 atattattgataaaataacaagtcaggtattattagtcgaacgaacaaataattttt 180
 Qy 181 gatgcaagtttaaaatcagaataatttcaaaactgattatatacagctggtagctgcg 240
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 181 gatgcaagtttaaaatcagaataatttcaaaactgattatatacagctggtagctgcg 240
 Qy 241 tagatgaagactgagtcgtagattattgttaatacataaaattgatgatagtagctt 300
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 241 tagatgaagactgagtcgtagattattgttaatacataaaattgatgatagtagctt 300

Db 2460 gtaataaaaaataataatctattgtctgaaattatctcagatgtttaagattttctttaagta 2519
QY 2521 aattctttcaaaatttagctaaagctctgttaataactaaagaataatacacacatctcga 2580
Db 2520 aattctttcaaaatttagctaaagctctgttaataactaaagaataatacacacatctcga 2579
QY 2581 ccacgaaaaaaacacataataaaattgaaatttcgacccggtaccccggaattcgagct 2640
Db 2580 ccacgaaaaaaacacataataaaattgaaatttcgacccggtaccccggaattcgagct 2639
QY 2641 cggtaaccggggaattcccgatctagtaacatagatgacacgcgcgcgataatttacc 2700
Db 2640 cggtaaccggggaattcccgatctagtaacatagatgacacgcgcgcgataatttacc 2699
QY 2701 ctagtttgcgcgtatatttggttttctctacgcgtatctaaattgataattgcgggactct 2760
Db 2700 ctagtttgcgcgtatatttggttttctctacgcgtattaaattgataattgcgggactct 2759
QY 2761 aatcataaaaccctctcataataaacgctcatgcattacatgtttaatttaccatgctt 2820
Db 2760 aatcataaaaccctctcataataaacgctcatgcattacatgtttaatttaccatgctt 2819
QY 2821 aacgtaattcaacagaaattatgatataatcatcgcaagaccgcgaacagattcaatct 2880
Db 2820 aacgtaattcaacagaaattatgatataatcatcgcaagaccgcgaacagattcaatct 2879
QY 2881 taagaaactttatgccaatgtttgaacgatctgttcggatccctctagagcgggaaag 2940
Db 2880 taagaaactttatgccaatgtttgaacgatctgttcggatccctctagagcgggaaag 2939
QY 2941 tgaattgaccgatcagagtttgaagaaaaattatttacacattttatgtaaagctgaaa 3000
Db 2940 tgaattgaccgatcagagtttgaagaaaaattatttacacattttatgtaaagctgaaa 2999
QY 3001 aaaaagcctcccgaggaaagccgttttttcggttatctgatttttgaaggctgataa 3060
Db 3000 aaaaagcctcccgaggaaagccgttttttcggttatctgatttttgaaggctgataa 3059
QY 3061 tggctcggttgttttgaatacagccagctgttgagtaaaagaaatccggtctgaattctg 3120
Db 3060 tggctcggttgttttgaatacagccagctgttgagtaaaagaaatccggtctgaattctg 3119
QY 3121 aagcctgatgatatagttaataatccgcttcacgcaatgttgcgtccgcttttgcgcggag 3180
Db 3120 aagcctgatgatatagttaataatccgcttcacgcaatgttgcgtccgcttttgcgcggag 3179
QY 3181 ttgccttccctgtttgagaagatgtctccgcgatgcttttcccccgcgagcagctcgca 3240
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QY 3241 aggttcccttttgatgccacccagcgagggttgtgcttctgattttgtaagttaatta 3300
Db 3240 aggttcccttttgatgccacccagcgagggttgtgcttctgattttgtaagttaatta 3299
QY 3301 tcagggtagcttatgatgtctgaagataatccgcgaaccocgccaacgctgttgataacc 3360
Db 3300 tcagggtagcttatgatgtctgaagataatccgcgaaccocgccaacgctgttgataacc 3359
QY 3361 ggtaccatggtagtaattcttctaagtaaaactttgatttttgagtgatgtgttgact 3420
Db 3360 ggtaccatggtagtaattcttctaagtaaaactttgatttttgagtgatgtgttgact 3419
QY 3421 gttacacttgcacaaagggcataatagagcacagacatacacacaacacttgcaaaa 3480
Db 3420 gttacacttgcacaaagggcataatagagcacagacatacacacaacacttgcaaaa 3479
QY 3481 ctaactttgttgagcaatttcgagaaaaatggggagtagcaggctaaacttgaggggtaac 3540
Db 3480 ctaactttgttgagcaatttcgagaaaaatggggagtagcaggctaaacttgaggggtaac 3539
QY 3541 attaaaggtttcatgtaattattgttgcaaacatggacttagtgtgagggaaaaagtacca 3600
Db 3540 attaaaggtttcatgtaattattgttgcaaacatggacttagtgtgagggaaaaagtacca 3599

QY 3601 aaattttgtctccacctgatttcagtttatggaaattacattatgaagctgtgctagaaa 3660
Db 3600 aaattttgtctccacctgatttcagtttatggaaattacattatgaagctgtgctagaaa 3659
QY 3661 gatgtttattctctagtcagccacccacccttatgcaagctgtgcttttagcttgattcaaaa 3720
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QY 3721 acgatttaatttacattgctaaaatgtgcatacttcgagcctatgtcgctttaaattcgag 3780
Db 3720 acgatttaatttacattgctaaaatgtgcatacttcgagcctatgtcgctttaaattcgag 3779
QY 3781 taggatgtatatattagtcataaaaaatcatgttttgaatcatctttcataaaagtacaa 3840
Db 3780 taggatgtatatattagtcataaaaaatcatgttttgaatcatctttcataaaagtacaa 3839
QY 3841 gtcaattgtcccttcttggtttggcacctatatccaatctgtttaatgtcaaaattatccaatta 3900
Db 3840 gtcaattgtcccttcttggtttggcacctatatccaatctgtttaatgtcaaaattatccaatta 3899
QY 3901 tacttagctagatatccaattttgaaataaaaatagctcttgcattagtaaaacccgagatgtg 3960
Db 3900 tacttagctagatatccaattttgaaataaaaatagctcttgcattagtaaaacccgagatgtg 3959
QY 3961 acaaaagtcacatatccaatcaaaacttctggtgctgtggtggttaagtcttgatcgacatgggg 4020
Db 3960 acaaaagtcacatatccaatcaaaacttctggtgctgtggtggttaagtcttgatcgacatgggg 4019
QY 4021 ttaaaatttaaaatgggacacataaaatagctatttggcaaatctcccctatcgaaatg 4080
Db 4020 ttaaaatttaaaatgggacacataaaatagctatttggcaaatctcccctatcgaaatg 4079
QY 4081 acagattgttcacatggaatacaaaaaagctcctctgatagaagtcgcaaaagtatcacaaatt 4140
Db 4080 acagattgttcacatggaatacaaaaaagctcctctgatagaagtcgcaaaagtatcacaaatt 4139
QY 4141 tctatcgagagatagattgaaagaagtgcagggaagcggttaactggaacatacaacaat 4200
Db 4140 tctatcgagagatagattgaaagaagtgcagggaagcggttaactggaacatacaacaat 4199
QY 4201 gtctaaattaaatgcattctgcataaccaaaaaagtgatatctactctctccgggtcccaataag 4260
Db 4200 gtctaaattaaatgcattctgcataaccaaaaaagtgatatctactctctccgggtcccaataag 4259
QY 4261 ttattttttggcccttttttatgtgtccaaaaataagtgtgttttttagatttcaaaaaatg 4320
Db 4260 ttattttttggcccttttttatgtgtccaaaaataagtgtgttttttagatttcaaaaaatg 4319
QY 4321 atttaattattttttactacagtgccttggagtaaatgggtgtgtgagtagtgttgaatg 4380
Db 4320 atttaattattttttactacagtgccttggagtaaatgggtgtgtgagtagtgttgaatg 4379
QY 4381 aatgtttatgtgaagaataatagtaaaaggttaatatgtacaaatttcoatttgcattttaaagtt 4440
Db 4380 aatgtttatgtgaagaataatagtaaaaggttaatatgtacaaatttcoatttgcattttaaagtt 4439
QY 4441 aaaaatgtaatttcttaattctgtgtgaatacaacacaaaaaacacttatttgggaccgga 4500
Db 4440 aaaaatgtaatttcttaattctgtgtgaatacaacacaaaaaacacttatttgggaccgga 4499
QY 4501 gaaagtataaaaaatatatttgggaagcgactaaaaataaaacttttctcatattatcaga 4560
Db 4500 gaaagtataaaaaatatatttgggaagcgactaaaaataaaacttttctcatattatcaga 4559
QY 4561 acctaaaaacagacataatggtagtttcttagggaatcttaaatcaactaaaaatataaaaaagaa 4620
Db 4560 acctaaaaacagacataatggtagtttcttagggaatcttaaatcaactaaaaatataaaaaagaa 4619
QY 4621 gcaacaagtatcaatacatatgatttacacgcgtcaaacgcgaagaaattcgtaaaaatttaatt 4680
Db 4620 gcaacaagtatcaatacatatgatttacacgcgtcaaacgcgaagaaattcgtaaaaatttaatt 4679

[illegible]

PT Maintainer gene for maintenance of male-sterile plants -
 PT comprises fertility-restorer gene and pollen-lethality gene
 XX
 PS
 PS
 XX Example 2; Page 55-58; 87pp; English.

CC A maintainer gene of plants, pref. a foreign chimeric gene,
 CC comprises (a) a fertility restorer gene which comprises a fertility
 CC restorer DNA and (ii) a restorer promoter capable of
 CC directing the expression of the fertility restorer DNA and (b) a
 CC pollen lethality gene that is selectively expressed in microspores
 CC and/or pollen of the plant to prevent the production of functional
 CC pollen and which comprises (i) a pollen lethality DNA and (ii) a
 CC pollen specific promoter capable of directing expression of the
 CC pollen lethality DNA. Plants transformed with this DNA (maintainer
 CC plants) can be used to maintain a homogenous population of male
 CC sterile plants for the production of hybrid seed. This plasmid
 CC contains DNA encoding Barnase (the pollen lethality DNA), the TA29
 CC tapetum-specific promoter (the restorer promoter) and
 CC phosphinothricin acetyl transferase under the control of the 35S3
 CC promoter. It was used alongside another plasmid (pVE144, described
 CC in file AA053874) in the construction of a plant transformation vector
 CC comprising a maintainer gene as described.
 XX
 SQ

Sequence 5620 BP; 1499 A; 1362 C; 1324 G; 1431 T; 4 other;

Query Match 21.6%; Score 1267.2; DB 15; Length 5620;
 Best Local Similarity 98.7%; Pred. No. 2.9e+203;
 Matches 1289; Conservative 0; Mismatches 13; Indels 4; Gaps 1;

QY 2612 ttctgacccggtaccgggaattcgactcggtaccggggatctcccgatctagtaac 2671
 DB | | | | |
 QY 378 tgtaaaacgacgcgcagtgattcgactcggtaccggggatctcccgatctagtaac 437
 DB | | | | |
 QY 2672 atagatgacccgcgcgataattctatctagtttgcgcgtatatttggttctatc 2731
 DB | | | | |
 QY 438 atagatgacccgcgcgataattctatctagtttgcgcgtatatttggttctatc 497
 DB | | | | |
 QY 2732 gcgtattaaatgataattcgggactctaatcataaaacccctcataaaataacgctc 2791
 DB | | | | |
 QY 498 gcgtattaaatgataattcgggactctaatcataaaacccctcataaaataacgctc 557
 DB | | | | |
 QY 2792 atgcattacatgttaattatatacattgtaacgttaattcaacgagaattatgatgaatc 2851
 DB | | | | |
 QY 558 atgcattacatgttaattatatacattgtaacgttaattcaacgagaattatgatgaatc 617
 DB | | | | |
 QY 2852 atcgcgaagccgcgaacagagattcaattctaaagaaacttattgccaaatgtttgaacga 2911
 DB | | | | |
 QY 618 atcgcgaagccgcgaacagagattcaattctaaagaaacttattgccaaatgtttgaacga 677
 DB | | | | |
 QY 2912 tctgcttcggtatctctctagag- ---ccggaagtgaaatgaccgatcagagtttgaaga 2967
 DB | | | | |
 QY 678 tctgcttcggtatctctctagagnnnccggaagtgaaatgaccgatcagagtttgaaga 737
 DB | | | | |
 QY 2968 aaaaattattacacattttatgataagctgaaaaaaacgacctccgcgagaagcgtttt 3027
 DB | | | | |
 QY 738 aaaaattattacacattttatgataagctgaaaaaaacgacctccgcgagaagcgtttt 797
 DB | | | | |
 QY 3028 ttccgttatctgattttgttaaaggctcgataatggtccctgtttgttaaatacagcag 3087
 DB | | | | |
 QY 798 ttccgttatctgattttgttaaaggctcgataatggtccctgtttgttaaatacagcag 857
 DB | | | | |
 QY 3088 tcgcttgagtaaaagatacccggtctgaaattctgaagcctgatgtatagtaataatccgct 3147
 DB | | | | |
 QY 858 tcgcttgagtaaaagatacccggtctgaaattctgaagcctgatgtatagtaataatccgct 917
 DB | | | | |
 QY 3148 tcaogccatgttcgctcgtttttgcccggagtttgccttccctgtttgagaagatgtct 3207
 DB | | | | |
 QY 918 tcaogccatgttcgctcgtttttgcccggagtttgccttccctgtttgagaagatgtct 977
 DB | | | | |
 QY 3208 ccgcccagatgttttcccccggagcagctctgcaaggttccctttttgatgccaccacgccc 3267
 DB | | | | |
 QY 978 ccgcccagatgttttcccccggagcagctctgcaaggttccctttttgatgccaccacgccc 1037
 DB | | | | |

QY 3268 agggcttgcttctctgattttgtaattatcaggtagcttatgatgtctgaaga 3327
 DB | | | | |
 QY 1038 agggcttgcttctctgattttgtaattatcaggtagcttatgatgtctgaaga 1097
 DB | | | | |
 QY 3328 taatccgcaaaccccgctcaaacgctgttgataaccggtaccatggtagtaattttttaag 3387
 DB | | | | |
 QY 1098 taatccgcaaaccccgctcaaacgctgttgataaccggtaccatggtagtaattttttaag 1157
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 QY 3388 taaaaactttgatttgatgattgattgttactgttacactgcaccacaaggcatata 3447
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 QY 1158 taaaaactttgatttgatgattgattgttactgttacactgcaccacaaggcatata 1217
 DB | | | | |
 QY 3448 tagagcaagacacatacacacaacttgcaaaactcttttggagcaatttcgagga 3507
 DB | | | | |
 QY 1218 tagagcaagacacatacacacaacttgcaaaactcttttggagcaatttcgagga 1277
 DB | | | | |
 QY 3508 aaatggggagtagcagcgttaactctgagggtaacatttaagggtttcatttaattttgtg 3567
 DB | | | | |
 QY 1278 aaatggggagtagcagcgttaactctgagcctaacttaagggtttcatttaattttgtg 1337
 DB | | | | |
 QY 3568 caaacatggacttagtgaggaagaaagtaacaaaattttgtctcacctgatttcagtt 3627
 DB | | | | |
 QY 1338 caaacatggacttagtgaggaagaaagtaacaaaattttgtctcacctgatttcagtt 1397
 DB | | | | |
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 DB | | | | |
 QY 1398 atggaattacattatgaagctgtctgagagaagatgtttattcttagtccagccacccac 1457
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 QY 3688 ctatgcaagctcgtcttttagcttgattgattcaaaaactgatttaattacattgcataatgt 3747
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 QY 1458 ctatgcaagctcgtcttttagcttgattgattcaaaaactgatttaattacattgcataatgt 1517
 DB | | | | |
 QY 3748 gcatacttcgagcctatgtcgccttaattcgcagtagatgtatatattagcacataaaaa 3807
 DB | | | | |
 QY 1518 gcatacttcgagcctatgtcgccttaattcgcagtagatgtatatattagcacataaaaa 1577
 DB | | | | |
 QY 3808 atcatgtttgaatcatcttctcattcaaaagtgacaagtcgaattgcctctcttctgttggcact 3867
 DB | | | | |
 QY 1578 atcatgtttgaatcatcttctcattcaaaagtgacaagtcgaattgcctctcttctgttggcact 1637
 DB | | | | |
 QY 3868 atattcaatctgttaattgcaaaattatccagttatcattagctagatagat 3913
 DB | | | | |
 QY 1638 atattcaatctgttaattgcaaaattatccagttatcattagctagatagat 1683
 DB | | | | |
 RESULT 6
 AAV23239
 ID - AAV23239 standard; DNA; 5349 BP.
 XX
 AC AAV23239;
 XX
 XX
 DT 17-JUL-1998 (first entry)
 XX
 DE T-DNA of pTTS24.
 XX
 KW Barstar; barnase inhibitor; fertility restoration;
 KW male-sterile line; plasmid pTTS24; T-DNA; ds.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature complement (1..25)
 FT /*tag= a
 FT /label= RB
 FT /note= "right boarder"
 FT 3'UTR complement (98..331)
 FT /*tag= b
 FT /label= 3'-g7
 FT /note= "region containing 3' untranslated end of
 FT CDS Agrobacterium T-DNA gene 7"
 FT 332..883
 FT /*tag= c

CC Plasmid pTS172 (AA761394) contains the barnase coding sequence under
CC control of the rice El gene stamen-specific promoter and a
CC phosphinothricin acetyltransferase coding sequence under control of
CC the CamV 35S promoter. Plasmid pTS172 and plasmid pTS172 (see also
CC AA761395) were used to transform wheat Spring variety Pavon calli via
CC particle bombardment. Some calli were treated with the poly-(ADP-
CC ribose) polymerase inhibitor niacinamide before, or before and
CC after, bombardment. Healthy, male sterile plants were regenerated
CC only from bombarded calli that were treated with niacinamide. This
CC was believed to be due to more faithful expression characteristics
CC of the integrated stamen-selective barnase gene in these calli
CC and regenerated shoots. For plants transformed with pTS172,
CC foreign DNA was stably incorporated in the wheat genome in 2-3
CC copies.
XX
SQ Sequence 6548 BP; 1756 A; 1579 C; 1523 G; 1690 T; 0 other;

Query Match 14.2%; Score 832.8; DB 18; Length 6548;
Best Local Similarity 99.8%; Pred. No. 1.3e-130;
Matches 834; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 54 gtacatggtcgaataaagagcaattgttagatgtttaattcccatcttgaagaataat 113
DB 6540 GTACATGTCGATGAAGAAAGGCAATTTGTAGATGTTAATTCCTTGAAGAAATAT 6481

QY 114 agtttaaatatttattgataaaataacaagtcaggtattatagtcgaagcaaaacataa 173
DB 6480 AGTTTAAATATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAACATAA 6421

QY 174 atttattgatgcaagtttaattcagaataatttccaactgattatatacagctggtac 233
DB 6420 ATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGTAC 6361

QY 234 attgcctagatgaagactgagtcgcatattatgtgtaacataaattgatgatag 293
DB 6360 ATTGCGGTAGATGAAGACATGAGTCGCATATTATGTGTATACATAAATTTGATGATATAG 6301

QY 294 ctagcttagctatcggtgggatacctagaacgcgtgatctcagatctcggtgacggcgag 353
DB 6300 CTAGCTTAGCTATCGGGGGATCCTAGAACGCGTGATCTCAGATCTCGGTGACGGCAGG 6241

QY 354 acggaacgggggtaccgcgaagtcgaagtcagctgcagaaacccacgtatgcag 413
DB 6240 ACCGGACGGGGCGGTACCGCGCAGGCTGAAGTCCAGCTGCCAGAAACCCAGCTCATGCCAG 6181

QY 414 ttcccgctgtgaagccggccgcgcagcatgcgcggggggcattatccgagcgccctcg 473
DB 6180 TTCCCGTGTGAAGCGGGCCGCCGAGCATGCCGGGGGGCATATCCGAGGCGCTCG 6121

QY 474 tgcagcgacgctcggtgtgtgtggcagccgcatgatgacagccagcgtcttgaagccc 533
DB 6120 TGCATGCCACGCTCGGGTGTGTGGGCGAGCCGATGACAGCAGCACGCTCTTGAAGCCC 6061

QY 534 tgtgctccaggaacttcagcaggtgggttagagcgtgagccccagtcgcgtg 593
DB 6060 TGTGCTCCAGGGAATTCACGAGGTGGGTGTAGAGCGTGGAGCCCACTGCCGTCCCGTGG 6001

QY 594 tggcgggggagacgtacacggtcgactcgccgctcagtcgtaggcgttcgctgcttc 653
DB 6000 TGCGGGGGGAGAGCTACACGCTGACTCGGCCCTCCAGTCGTAGGCGTGTTCGCTGCCCTTC 5941

QY 654 caggggcccgtaggcagtgccgggacactcgccgtccacctcggcagcagcagcagga 713
DB 5940 CAGGGGGCCGGTAGGCGATGCCGGCACTCGCCGTCACCTCGGGCGACGAGCCAGGA 5881

QY 714 tagcgtcccgacagcagcaggtctcccgctccactccctcggttccctgcggtcgta 773
DB 5880 TAGCGCTCCCGCAGCAGCGAGCGAGGTCTCGCTCCGCTCCACTCCCTGCGGTTCCTCGGGCTCGGTA 5821

QY 774 cgaagttgacctgctgtcgtatagttggttagcagtggtgagacgcgcggcatg 833
DB 5820 CGGAAGTTGACCGGCTGTGCTCGATGTAGTGGTTGACGATGGTGGCAGACCGCGCGCATG 5761

QY 834 tccgcctcgtgtgcaocggcgagatgtcgccggcgctgcttctgggtccattgttct 889
DB 5760 TCCGCTCGGTGGCAGCGCGGATGTCCGGCGGGCGTCTGCTGGTCCATGGTTAT 5705

RESULT 10
AAZ91096/c
ID AAZ91096 standard; DNA; 6548 BP.
XX
AC AAZ91096;
XX
DT 06-JUN-2000 (first entry)
XX
DE E. coli plasmid pTS172 containing synthetic barnase gene.
XX
KW Male sterile plant; mutant barnase gene; anther-specific expression;
KW low fidelity PCR; primer; plant breeding; ss.
XX
OS Synthetic.
XX
PN WO200008176-Al.
XX
PD 17-FEB-2000.
XX
PF 03-AUG-1999; 99WO-JP04167.
PR 04-AUG-1998; 98JP-0220060.
XX
PA (NISR) JAPAN TOBRACCO INC.
XX
PI Hamada K, Nakakido F;
XX
DR WPI; 2000-195581/17.
XX
PT Mutate barnase gene for efficient construction of plant transformants,
PT particularly male sterile plants free from any undesirable characters
PT by specifically expressing the gene alone in anther .
XX
PS Example 3; Page 19-23; 30pp; Japanese.
XX
CC The invention relates to the generation of male sterile plants by
CC the introduction of a mutant barnase gene (AAZ91095) for expression
CC specifically in the anther of a plant. This sequence represents the
CC E. coli/Agrobacterium shuttle vector plasmid pTS172 which contains
CC the synthetic barnase gene (AAZ91094) under control of the cauliflower
CC mosaic virus 35S promoter. The vector also contains a region of the
CC Agrobacterium T-DNA gene 7. The vector is used for transmitting the
CC barnase gene to plants via an Agrobacterium tumefaciens host cell.
CC The transformed plant is used in plant breeding.
XX
SQ Sequence 6548 BP; 1756 A; 1579 C; 1523 G; 1690 T; 0 other;

Query Match 14.2%; Score 832.8; DB 21; Length 6548;
Best Local Similarity 99.8%; Pred. No. 1.3e-130;
Matches 834; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 54 gtacatggtcgaataaagagcaattgttagatgtttaattcccatcttgaagaataat 113
DB 6540 GTACATGTCGATGAAGAAAGGCAATTTGTAGATGTTAATTCCTTGAAGAAATAT 6481

QY 114 agtttaaatatttattgataaaataacaagtcaggtattatagtcgaagcaaaacataa 173
DB 6480 AGTTTAAATATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAACATAA 6421

QY 174 atttattgatgcaagtttaattcagaataatttccaactgattatatacagctggtac 233
DB 6420 ATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGTAC 6361

QY 234 attgcctagatgaagactgagtcgcatattatgtgtaacataaattgatgatag 293
DB 6360 ATTGCGGTAGATGAAGACATGAGTCGCATATTATGTGTATACATAAATTTGATGATATAG 6301


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Qy 826 ccggcatgcgcctcggtggcagcgcgatgtcgccggcgctcgcttctgggtccattg 885
Db 5988 CCGGCATGTCGGCTCGGTGGCACGGCGGATGTCGGCGGGCGTCTTGGGCTCATGG 5929
Qy 886 ttcttcttt 894
Db 5928 ATCCGATT 5920

RESULT 12
AAT39338
ID AAT39338 standard; DNA; 3658 BP.
XX
AC AAT39338;
XX
DT 22-JAN-1997 (first entry)
XX
DE Plasmid pVE136 (EcoRI-HindIII fragment).
XX
KW Plasmid pVE136; male sterile; barnase; ribonuclease; barstar;
KW transgenic plant; maize; corn; Zea mays; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..26
FT FT /*tag= a
FT FT /label= pUC19
FT FT /note= "polylinker of pUC19"
FT FT complement (28..403)
FT FT /*tag= b
FT FT /label= 3'nos
FT FT /note= "region containing polyA signal of
FT FT Agrobacterium T-DNA nopaline synthase gene"
FT FT complement (404..739)
FT FT /*tag= c
FT FT /label= Barnase
FT FT /note= "Bacillus amyloliquefaciens barnase coding
FT FT region"
FT FT complement (740..1918)
FT FT /*tag= d
FT FT /label= PCA55
FT FT /note= "maize CA55 gene promoter"
FT FT 1956..2788
FT FT /*tag= e
FT FT /label= p35S
FT FT /note= "cauliflower mosaic virus 35S promoter"
FT FT 2789..3340
FT FT /*tag= f
FT FT /label= bar
FT FT /note= "phosphinothricin acetyltransferase coding
FT FT region"
FT FT 3341..3623
FT FT /*tag= g
FT FT /label= 3'nos
FT FT /note= "region containing polyA signal of
FT FT Agrobacterium T-DNA nopaline synthase gene"
FT FT 3624..3658
FT FT /*tag= h
FT FT /label= pUC19
FT FT /note= "polylinker of pUC19"
FT FT
XX
PN WO9626283-A1.
XX
XX 29-AUG-1996.
XX
XX 21-FEB-1996; 96WO-EP00722.
XX
XX 21-FEB-1995; 95EP-0400364.
XX
XX (PLBZ ) PLANT GENETIC SYSTEMS NV.
XX
PI Botterman J, Cornelissen M, Michiels F;
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XX WPI; 1996-402373/40.
XX
XX Prodn. of male sterile plants by transforming with a chimaeric
XX construct "comprising a male sterility DNA e.g. barnase and a
XX co-regulating gene, e.g. barstar, into the nuclear genome, useful
XX for generating hybrid cultivars
XX
XX Example 2; Page 40-42; 56pp; English.
XX
XX The EcoRI-HindIII fragment (AAT39338) of plasmid pVE136 contains
XX a Bacillus barnase (ribonuclease) gene under control of the PCA55
XX promoter. Embryogenic callus from maize was transformed with
XX pVE136 and pTS88 (see also AAT39337), a pGEM2-derived plasmid contg.
XX barstar DNA under control of a 35S promoter. Maize plants contg.
XX both p35S-barstar-3'g7 and the PCA55-barnase-3'nos chimeric genes
XX were male sterile. Foreign genes such as barnase can be placed
XX under control of a stamen-specific promoter to produce male sterile
XX plants; constitutive expression of barstar counteracts any low
XX level expression of barnase in other tissues.
XX
XX Sequence 3658 BP; 1050 A; 857 C; 797 G; 954 T; 0 other;
XX
XX
XX Query Match 12.6%; Score 741.8; DB 17; Length 3658;
XX Best Local Similarity 99.7%; Pred. No. 1.9e-115;
XX Matches 743; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 2630 gaattcgagctcggtaccgccgggatcttcccgatcttagtaacatagatgacacgcgcgc 2689
Db 1 gaattcgagctcggtaccgccgggatcttcccgatcttagtaacatagatgacacgcgcgc 60
Qy 2690 gataattatctagttgcgcgtatatattgtttctatcgcgtattaaatgtataat 2749
Db 61 gataattatctagttgcgcgtatatattgtttctatcgcgtattaaatgtataat 120
Qy 2750 tgcgggactctaataaaacccatctcataataaacgtcatgcatcattgttaatt 2809
Db 121 tgcgggactctaataaaacccatctcataataaacgtcatgcatcattgttaatt 180
Qy 2810 attacatgcttaacgtaattcaacagaaattatatgataatcgcgaagccggcaaca 2869
Db 181 attacatgcttaacgtaattcaacagaaattatatgataatcgcgaagccggcaaca 240
Qy 2870 ggattcaatcttaagaaactttattgccaaatgtttgaacgatctgctcgatcctcta 2929
Db 241 ggattcaatcttaagaaactttattgccaaatgtttgaacgatctgctcgatcctcta 300
Qy 2930 gacccgaaagtgaattgaccgatcagagtttgaagaaaaattattacacactttatg 2989
Db 301 gacccgaaagtgaattgaccgatcagagtttgaagaaaaattattacacactttatg 360
Qy 2990 taaagctgaaaaaacgcccgcaggaaagccgttttttcgttatctgattttgttaa 3049
Db 361 taaagctgaaaaaacgcccgcaggaaagccgttttttcgttatctgattttgttaa 420
Qy 3050 aggtctgataatggtccgtttttttgtaaatcagccagctcgttgagtaaaagaaatccggt 3109
Db 421 aggtctgataatggtccgtttttttgtaaatcagccagctcgttgagtaaaagaaatccggt 480
Qy 3110 ctgaatttctgaagcctgatgtatagtttaataatccggttcacgcacatgttgcgcgtttt 3169
Db 481 ctgaatttctgaagcctgatgtatagtttaataatccggttcacgcacatgttgcgcgtttt 540
Qy 3170 tgcggggagtttgccttccctgtttgagaagatgtctccgcgatgcttttcccgagag 3229
Db 541 tgcggggagtttgccttccctgtttgagaagatgtctccgcgatgcttttcccgagag 600
Qy 3230 cgacgctcgaaggttccctttttgatgccaccgcagcgaggttctgtctctgattttg 3289
Db 601 cgacgctcgaaggttccctttttgatgccaccgcagcgaggttctgtctctgattttg 660
Qy 3290 taatgtaattatcaggttagcttatgatatgtctgaagataatccgcaaaccccgctcaaacg 3349
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Db 661 taaatgaatcaggtagcttatgatctgtaagataatccgcaacccgtcaaacg 720
Qy 3350 tgttgataacccggtaccatggtagc 3374
Db 721 tgttgataacccggtaccatggtgc 745

RESULT 13
AAQ53889
ID AAQ53889 standard; DNA; 4808 BP.
XX
AC AAQ53889;
XX
DT 27-JUN-1994 (first entry)
XX
DE Restriction fragment of construct carrying plant maintainer gene.
XX
KW Maintainer gene; sterile; sterility; homogenous population; hybrid;
KW seed; fertility restorer gene; pollen lethality gene; ss.
OS Synthetic.
XX
FH Key
FT misc_signal
FT complement (18..401)
FT /tag= a
FT /label= 3' nos.
FT /note= "3' regulatory sequence containing the
FT polyadenylation site derived from
FT Agrobacterium T-DNA nopaline synthase gene."
FT
CDS
FT complement (402..737)
FT /tag= b
FT /label= Barnase.
FT /note= "Coding region of the barnase gene of
FT Bacillus amyloliquefaciens."
FT
promoter
FT complement (738..1944)
FT /tag= c
FT /label= PZM13.
FT /note= "Promoter region of the Zm 13 gene of Zea
FT mays."
FT
misc_signal
FT complement (1945..2281)
FT /tag= d
FT /label= 3' nos.
FT
CDS
FT complement (2282..2554)
FT /tag= e
FT /label= Barstar.
FT /note= "Coding region of the barstar gene of
FT Bacillus amyloliquefaciens."
FT
promoter
FT complement (2555..3099)
FT /tag= f
FT /label= PTA29.
FT /note= "Promoter region of the TA29 gene of
FT Nicotiana tabacum."
FT
promoter
FT 3100..3932
FT /tag= g
FT /label= 35S3.
FT /note= "35S3" promoter sequence derived from
FT cauliflower mosaic virus isolate CabbB-JI."
FT
CDS
FT 3933..4484
FT /tag= h
FT /note= "Coding region of the phosphinothricin
FT acetyltransferase gene."
FT
misc_signal
FT 4485..4763
FT /tag= i
FT /label= 3' nos.
XX
W09325695-A.
XX
23-DEC-1993.
XX
11-JUN-1993; 93WO-EP01489.
XX
12-JUN-1992; 92US-0899072.
PR

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PR 03-NOV-1992; 92US-0970840.
XX
PA (PLBZ ) PLANT GENETIC SYSTEMS NV.
XX
PI Leemans J, Williams M;
XX
DR WPT; 1994-007552/01.
XX
PT Maintainer gene for maintenance of male-sterile plants -
PT comprises fertility-restorer gene and pollen-lethality gene
XX
PS Example 2; Page 73-75; 87pp; English.
XX
CC A maintainer gene of plants, pref. a foreign chimeric gene,
CC comprises (a) a fertility restorer gene which comprises a fertility
CC restorer DNA and (ii) a restorer promoter capable of
CC directing the expression of the fertility restorer DNA and (b) a
CC pollen lethality gene that is selectively expressed in microspores
CC and/or pollen of the plant to prevent the production of functional
CC pollen and which comprises (i) a pollen lethality DNA and (ii) a
CC pollen specific promoter capable of directing expression of the
CC pollen lethality DNA. Plants transformed with this DNA (maintainer
CC plants) can be used to maintain a homogenous population of male
CC sterile plants for the production of hybrid seed. This sequence is
CC an EcoRI-HindIII restriction fragment of the construct designated
CC pT5218 and comprises the maintainer gene described.
XX
SQ Sequence 4808 BP; 1370 A; 1064 C; 1037 G; 1333 T; 4 other;

Query Match 12.4%; Score 727.8; DB 15; Length 4808;
Best Local Similarity 99.2%; Pred. NO. 4.4e-113;
Matches 743; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

Qy 2630 gaattcgagctggtaccggggtctcccgatctccgatctagtaacatagatgacacccggcgc 2689
Db 1 gaattcgagctggtaccggggtctcccgatctccgatctagtaacatagatgacacccggcgc 60
Qy 2690 gataattatctctagttgctgctatatattgttttctatcggtattaaatgataat 2749
Db 61 gataattatctctagttgctgctatatattgttttctatcggtattaaatgataat 120
Qy 2750 tgcgggactctaatcataaaaaaccatctcctataataacgctcatcattacatgtaatt 2809
Db 121 tgcgggactctaatcataaaaaaccatctcctataataacgctcatcattacatgtaatt 180
Qy 2810 attacatgcttaacgtaattcaacagaataattatgataataatcgcaagccggcaaca 2869
Db 181 attacatgcttaacgtaattcaacagaataattatgataataatcgcaagccggcaaca 240
Qy 2870 ggattcaattttaagaacattttattgcccatttgcgaatgtttgaacgatctgctcgatcctota 2939
Db 241 ggattcaattttaagaacattttattgcccatttgcgaatgtttgaacgatctgctcgatcctota 300
Qy 2930 gag----ccggaagtgaattgaccgatcagagtttgaaagaaaaattttatcacactt 2985
Db 301 gagnnnnccggaagtgaattgaccgatcagagtttgaaagaaaaattttatcacactt 360
Qy 2986 tatgtaaagctgaaaaaacgcctcccgaggaaagccgttttttctgtatctgattttt 3045
Db 361 tatgtaaagctgaaaaaacgcctcccgaggaaagccgttttttctgtatctgattttt 420
Qy 3046 gtaaaagctgataatggtccgtgtttttgtaatacagccagtcgcttgagtaagaatc 3105
Db 421 gtaaaagctgataatggtccgtgtttttgtaatacagccagtcgcttgagtaagaatc 480
Qy 3106 cggctgtaattctgaagcctgtagtatagttaataatccgctcaacccatgttcgtccg 3165
Db 481 cggctgtaattctgaagcctgtagtatagttaataatccgctcaacccatgttcgtccg 540
Qy 3166 cttttgccggggagtttgccttcctctgttttgagaagaatgtctccgcgatgtctttccccc 3225
Db 541 cttttgccggggagtttgccttcctctgttttgagaagaatgtctccgcgatgtctttccccc 600

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Db 2450 GCCTCCATTCCAAACGAGCGGGTACTCCACCCATCCGGT----- 2409

Qy 3168 ttgtccggggagtttgccttcctgtttgagaagatgtctcccgatgttcccccgg 3227

Db 2410 -----CAGACAATCCCATAAAGCGTCCAGGTTTTCACCGTAGTATTCGGGAAG 2363

Qy 3228 agcagctctgcaaggttcccttttggatgcccacccagcgaggttggcttctgtat 3287

Db 2362 GGC-----AAGCTCCTTTTCAATGCTGGTGGAGTGGCTGATCTCTGATTT 2313

Qy 3288 tgtaatgtaattatccaggttagctatgatatgctgaagataatccgcgaacccgtcaaa 3347

Db 2312 -----GTTCCCC 2306

Qy 3348 cgtgttgataacccgggtaccatgtagtaatttctttaaagtaaaactttgatttgatg 3407

Db 2305 GTTAATGACTGCTTTTTCATGTAGTAAATTTCTTAAAGTAAACCTTGATTGAGTG 2246

Qy 3408 atgatgtgtactgttacacttgcacacacaaagggtatatatagacacaaagacatacaca 3467

Db 2245 ATCATCTTGTACTGTTTACACTTGCACCAAGGGCATATATAGACACAAGACATACACA 2186

Qy 3468 acaactgcaaaactaaccttttggagcatttcgaggaataatggggagtagcaggcta 3527

Db 2185 ACAACTTGCAAAACCTAATCTTTGTTGGAGCATTTTCGAGGAAATGGGAGTAGCAGGCTA 2126

Qy 3528 atcgtgggtgaacattaaagtttcatgtatttaatttggtaaaacatggacttagtgta 3587

Db 2125 ATCTGAGGCTAACATTAAGTCTTCAATGATTAATTTGTTGCAACATGGACTTAGTGTA 2066

Qy 3588 ggaataagtaacaaatttgtctcacocctgatttcagttatggaaattacattatgaag 3647

Db 2065 GGAATAAGTACCAAAATTTGTCTCACCTGATTTTCAGTTATGGAATATCATATGAAG 2006

Qy 3648 ctgtgtgagagagatgtttattcttagtccagccacccaccccttatgcaagtctctttaa 3707

Db 2005 CTGTCTAGAGAGAGTGTATTCTTAGTCCAGCCACCCACCTTATGCAAGTCTGCTTTA 1946

Qy 3708 gcttattcaaaaactgatttaattacattgctaaatgtgcatacttcagccatagtc 3767

Db 1945 GCTTGATTTCAAAAACGTGATTAATTTACATTTGCTAAATGTCATCTTCGAGGCTATGTC 1886

Qy 3768 gcttcaatccagtaggtatgatatattagtaacataaaaaatcatgtttgaatcatcttt 3827

Db 1885 GCTTTAATTCAGTAGGATGTATATATAGTACATAAAAAATCATGTTTCAATCATCTTT 1826

Qy 3828 cataaagtaacagtcgaattgtcccttctgtttgttgacactatattcaatctgtaagca 3887

Db 1825 CATAAAGTGACAAGTCAATTTGCTCTTCTTTGTCACATATATTCATCTGTTAATGCA 1766

Qy 3888 aattatccagttataacttagtagat 3913

Db 1765 AATTATCCAGTTATACTTAGCTAGAT 1740

RESULT 15

AA15631/C

ID AAX15631 standard; DNA; 4896 BP.

AC AAX15631.

XX 07-MAY-1999 (first entry)

DE Nucleotide sequence of plasmid pTS256.

XX Cl gene; maize; male-sterile corn line; anthocyanin production;

KW pTS256; ds.

XX Synthetic.

OS US5880331-A.

PN 09-MAR-1999.

XX

PD

XX 07-JUN-1995; 95US-0485139.

PF 07-JUN-1995; 95US-0485139.

PR 06-JUN-1994; 94US-0254776.

XX (PLB2) PLANT GENETIC SYSTEMS NV.

PA Krebbers E, Leemans J, Williams M;

PI WPI; 1999-204053/17.

XX Process for maintaining a male-sterile corn line - using male

PT sterile plants lacking functional regulatory gene for anthocyanin

PS production

XX Example 2; Columns 31-36; 35pp; English.

XX The present sequence represents the nucleotide sequence of plasmid

CC pTS256. It is used in the course of the invention. The specification

CC describes a process for maintaining a male-sterile corn line, using male

CC sterile parent plants lacking a functional gene for anthocyanin

CC production, and a maintainer corn line comprising male fertile parent

CC plants containing foreign DNA comprising a restorer gene and an active

CC regulatory protein gene. By using the anthocyanin gene, the colour of

CC the male-sterile plants will differ from that of the male fertile

CC plants. This will enable the seeds harvested from the plants to be

CC easily separated into those that will grow into male-fertile plants and

CC those that will grow into male-sterile plants.

XX Sequence 4896 BP; 1251 A; 1147 C; 1186 G; 1312 T; 0 other;

Query Match 12.1%; Score 708.8; DB 20; Length 4896;

Best Local Similarity 76.6%; Pred. No. 6.6e-110;

Matches 985; Conservative 0; Mismatches 187; Indels 114; Gaps 5;

QY 2628 cggaaattcagctcgttacccgggattctccgcatctagtaacatagatgacacccgcg 2687

Db 2912 CAGAAATTCAGCTCGGTACCGGGGATCTCCGATCTAGTAACATAGATGACACCGGC 2853

QY 2688 gggataattatcctagtttgcgctatattttgttctatcgctattaaatgata 2747

Db 2852 GCGATAATTTATCTTATAGTTTGGCGCTATATTTGTTTCTATCGGTATTAATGTATA 2793

QY 2748 attgcggacttaatacaaaaaccatctcataaaacgtcatgacattgttaa 2807

Db 2792 ATTGCGGACTTATATATATAAAACCCATCTCATATAAATGATGATGATGATGATG 2733

QY 2808 ttattacatgcttaacgtaattcaacagaaattatgataatcatcgacacccgcaa 2867

Db 2732 TTATTACATGCTTAACGTAATTAACAGAAATTTATGATAATCATCGAAGACCGCAA 2673

QY 2868 caggattcaatctlaagaaactttattgcaaatgtttgaacgatctgttcgatactc 2927

Db 2672 CAGGATTCATCTTAAGAACTTTATTGCCAAATGTTTGAACGATCTGTTCGGATCCTC 2613

QY 2928 tagagccggaaagtgaattgacgatcagagtttgaagaaataattattacacactta 2987

Db 2612 TAGACCAAGCTTGGGGTGTGTTGTTCCATATT-----GTTCACTCCCATTTGAT 2563

QY 2988 tgtaaagctgaaaaaacgctccgcgaggaagccggttttttctgtatctgtattgt 3047

Db 2562 CGTATTAAAGAAAGTATGATGATGATGTCGAGCTTCCGCTTCCGCTTACGGAACCT 2503

QY 3048 aaaggtctgataatggctcgtttttgttaaatcaacagcagtcgcttgagtaagaatcgc 3107

Db 2502 GAAGCACACTCTCGGGCCATT-----TTCACTAGCTGCTTGTTCAAACT 2452

QY 3108 gctggaatttctgaagcctgtagtatagtaatatccgcttcacgcgatgttcgctcgcgt 3167

Db 2451 GCCTCCATTCCAAAACAGCGGGTACTCCACCATCCGGT----- 2410


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QY 3168 ttgcccggaggttgcttcctccctgtttgagaagatgtctcccgccgagtgcttttcccccg 3227
Db      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
2411 -----CAGACAATCCCAATAAAGCGTCAGGTTTTTCACCGTAGTATTCCGGAAG 2364
QY 3228 agcgacgtctgcgaaggtctcccttttgaatgcaccacccgagggcttgcttctctgattt 3287
Db      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
2363 GGC-----AAGCTCCTTTTTCAATGTCGGGCGAGTCCCTGATACTTCTGATTT 2314
QY 3288 tgaatgaattatcatcaggtagcttatgatatgtctgaagataatccgcaaccccgctcaaa 3347
Db      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
2313 -----GTTCCCC 2307
QY 3348 cgtgttgataaacccgggtaccatgtagctaattcttcttaagtaaaaaactttgatttgagtg 3407
Db      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
2306 GTTAATGACGTGCTTTTTTCATGTGTAGTAAATTTCTTTAAGTAAAAACTTTGATTGAGTG 2247
QY 3408 atgatgtgtactgttacacttcaccacaaagggcatatatagagcacagaacatacacaca 3467
Db      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
2246 ATGATGTTGTACTGTACACTTGCACCCACCAAGGGCATATATAGAGCACAAAGACATACACA 2187
QY 3468 acaacttgcaaaactaacttttgttgagcatttcggaggaataatggggagtagcaggcta 3527
Db      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
2186 ACRAACTTGCAAAACTAATTTTGTGGAGCATTTTCGAGGAAATGGGGAGTAGCAGGCTA 2127
QY 3528 atctgagggtaacattaaaggttccatgtatataatttgttgcaaacatgggacttagtgtga 3587
Db      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
2126 ATCTGAGGGTAACATTAAAGGTTTCATGTATTAATTTGTCAAACATGGACTTAGTGTGA 2067
QY 3588 ggaataagtaacaaaatttctcaccctgatttccagttatggaaaattacattatgaag 3647
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1946 GCTTGATTCAAAACCTGATTAAATTTACATTGCTAAATGTGCATACCTCGAGCCTATGTC 1887
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1766 AATTATCCAGTTATACCTAGCTAGAT 1741
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Job time: 15044 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2001, 16:22:28 ; Search time 154.69 Seconds
(without alignments)
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Title: US-09-698-903B-1
Perfect score: 5865
Sequence: 1 aattacaacggtatatcc.....caattgaatatctgcgcg 5865

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5843.4	99.6	5864	3	US-08-894-440-4
2	4903.2	83.6	4946	3	US-08-817-188-1
3	2386.8	40.7	5560	3	US-08-817-188-5
4	1270.4	21.7	5620	1	US-08-104-072B-9
5	1270.4	21.7	5620	1	US-08-351-413-3
6	1270.4	21.7	5620	2	US-09-025-583-3
7	1269	21.6	1287	1	US-08-064-121-3
8	1269	21.6	1287	1	US-08-478-015-3
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10	1269	21.6	1287	3	US-09-084-889-3
11	832.8	14.2	6548	3	US-08-817-188-2
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17	712	12.1	4896	3	US-08-750-357-2
18	708.8	12.1	4896	2	US-08-485-139-2
19	705.4	12.0	6376	1	US-08-104-073-5
20	705.2	12.0	6555	1	US-08-351-413-2
21	705.2	12.0	6555	2	US-09-025-583-2
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c 41	561.6	9.6	6376	1	US-08-104-073-5	Sequence 5, Appl
c 42	549	9.4	549	5	PCT-US91-0623A-1	Sequence 1, Appl
c 43	544.8	9.3	549	1	US-08-361-467B-10	Sequence 10, Appl
c 44	544.8	9.3	549	1	US-08-484-332C-10	Sequence 10, Appl
c 45	491.4	8.4	6548	3	US-08-894-440-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
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; Sequence 4, Application US/08894440
; Patent No. 6025546
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Method to obtain male sterile plants
; FILE REFERENCE: NMSCOR
; CURRENT APPLICATION NUMBER: US/08/894,440
; CURRENT FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
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; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: T-DNA of
; OTHER INFORMATION: plasmid pTCO113
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: right border of Agrobacterium T-DNA (RB)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((98)..(330))
; OTHER INFORMATION: region containing polyadenylation signal of gene 7
; OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((331)..(882))
; OTHER INFORMATION: region coding for phosphinothricin acetyl
; OTHER INFORMATION: transferase (bar)
; FEATURE:
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; LOCATION: Complement((883)..(2608))
; OTHER INFORMATION: promoter of small subunit gene of Rubisco of
; OTHER INFORMATION: Arabidopsis (Pssu)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((2659)..(3031))
; OTHER INFORMATION: region containing polyadenylation signal of
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; LOCATION: Complement((3032)..(3367))
; OTHER INFORMATION: region coding for barnase of Bacillus
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; OTHER INFORMATION: tabacum (PTA29)
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; LOCATION: (4924)..(5216)
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; OTHER INFORMATION: Agrobacterium T-DNA (Phos)
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; NAME/KEY: misc_feature
; LOCATION: Complement((5840)..(5864))
; OTHER INFORMATION: left border of Agrobacterium T-DNA
; US-08-894-440-4
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; OTHER INFORMATION: Description of Artificial Sequence: T-DNA of
; OTHER INFORMATION: plasmid pTHW107
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; NAME/KEY: misc_feature
; LOCATION: Complement(1)..(25))
; OTHER INFORMATION: T-DNA right border (RB)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement(97)..(330))
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; OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
; OTHER INFORMATION: T-DNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((331)..(882))
; OTHER INFORMATION: bar: region coding for phosphinotricin acetyl
; OTHER INFORMATION: transferase
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((883)..(2608))
; OTHER INFORMATION: promoter region of Rubisco small subunit gene of
; OTHER INFORMATION: Arabidopsis thaliana (PSSU)
; FEATURE:
; NAME/KEY: misc_feature
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; OTHER INFORMATION: gene of Agrobacterium T-DNA
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; US-08-817-188-1

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RESULT 3
US-08-817-188-5
; Sequence 5, Application US/08817188
; Patent No. 6074876
; GENERAL INFORMATION:
; APPLICANT: DE BLOCK, MARC
; TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
; FILE REFERENCE: 2121-0127P
; CURRENT APPLICATION NUMBER: US/08/817,188
; CURRENT FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: PCT/EP96/03366
; EARLIER FILING DATE: 1996-07-31
; EARLIER APPLICATION NUMBER: EP 95401844.6
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 5560
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: T-DNA of
; OTHER INFORMATION: plasmid pTHW142
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: RB: right border sequence of octopine TL-DNA from
; OTHER INFORMATION: pTiB6S3
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (84)..(296)
; OTHER INFORMATION: 3' g7: 3' untranslated region containing the
; OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (318)..(869)
; OTHER INFORMATION: bar: region coding for phosphinotricin
; OTHER INFORMATION: acetyltransferase
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (830)..(2760)
; OTHER INFORMATION: PSSU: promoter region of Rubisco small subunit
; OTHER INFORMATION: gene of Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2755)..(3058)
; OTHER INFORMATION: 3' untranslated region of the CaMV 35S transcript
; OTHER INFORMATION: containing polyadenylation signals
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3059)..(5056)
; OTHER INFORMATION: uidA: region coding for beta-glucuronidase
; FEATURE:
; NAME/KEY: misc_feature

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RESULT 4

US-08-104-072B-9
: Sequence 9, Application US/08104072B
: Patent No. 5639948
: GENERAL INFORMATION:
: APPLICANT: Michiels, Frank
: APPLICANT: Morloka, Sinji
: APPLICANT: Scheirlinck, Trees
: APPLICANT: Komari, Tosiniko
: TITLE OF INVENTION: Stamen-specific Promoters from Rice
: NUMBER OF SEQUENCES: 38
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Merchant & Gould
: STREET: 3100 No. 5639948west Center
: CITY: Minneapolis
: STATE: MN
: COUNTRY: USA
: ZIP: 55402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/104,072B
: FILING DATE: 05-AUG-1993
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO 9200272
: FILING DATE: 06-FEB-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: EP 91403352.7
: FILING DATE: 10-DEC-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: EP 91402590.3
: FILING DATE: 27-SEP-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: EP 91400318.1
: FILING DATE: 08-FEB-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Kowalchuk, Katherine M.
: REGISTRATION NUMBER: 36,848
: REFERENCE/DOCKET NUMBER: 8076.93USWO
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 612-332-5300
: TELEFAX: 612-332-9081
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5620 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: 1..395
: OTHER INFORMATION: /product= "pUC18 derived sequence"
: FEATURE:
: NAME/KEY: polyA_site
: LOCATION: 396..802
: OTHER INFORMATION: /standard_name= "from nopaline
: OTHER INFORMATION: synthase gene from Agrobacterium T-DNA"
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: NAME/KEY: promoter
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; FEATURE:
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; OTHER INFORMATION: /product= "CDS of phosphinotricin
; OTHER INFORMATION: acetyltransferase gene"
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; OTHER INFORMATION: /standard_name= "Agrobacterium
; OTHER INFORMATION: T-DNA nopaline synthase gene"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3357..5620
; OTHER INFORMATION: /product= "pUC18-derived sequence"
; US-08-104-072B-9
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Best Local Similarity 98.9%; Pred. No. 3e-268;
Matches 1291; Conservative 0; Mismatches 11; Indels 4; Gaps 1;
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RESULT 5
US-08-351-413-3
; Sequence 3, Application US/08351413
; Patent No. 5750867
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark
; APPLICANT: Leemans, Jan
; TITLE OF INVENTION: Maintenance of male-sterile plants
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 2046
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/351,413
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/899,072
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
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1 APPLICATION NUMBER: US 07/970,849
2 FILING DATE: 03-NOV-1992
3 ATTORNEY/AGENT INFORMATION:
4 NAME: Svensson, Leonard R.
5 REGISTRATION NUMBER: 30,330
6 REFERENCE/DOCKET NUMBER: 2121-102PCT
7 TELECOMMUNICATION INFORMATION:
8 TELEPHONE: (703) 205-8000
9 TELEFAX: (703) 205-8050
10 TELEX: 248345
11 INFORMATION FOR SEQ ID NO: 3:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 5620 base pairs
14 TYPE: nucleic acid
15 STRANDEDNESS: double
16 TOPOLOGY: circular
17 MOLECULE TYPE: DNA (genomic)
18 HYPOTHETICAL: NO
19 ANTI-SENSE: NO
20 ORIGINAL SOURCE:
21 ORGANISM: plasmid pVE108 (replicable)
22 FEATURE:
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26 OTHER INFORMATION: /note= "pUC18 der
27 FEATURE:
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33 OTHER INFORMATION: synthase gene fro
34 FEATURE:
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37 OTHER INFORMATION: /label= barnase
38 OTHER INFORMATION: /note= "coding re
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43 OTHER INFORMATION: /label= TA29
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Query Match

21.78; Score 1270.4; DB 1; Length 5620;

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RESULT 6

US-09-025-583-3
; Sequence 3, Application US/09025583
; Patent No. 5977433

: ORGANIZATION :
 : APPLICANT: Williams, Mark :
 : APPLICANT: Leemans, Jan :
 : TITLE OF INVENTION: Maintenance of male-sterile plants :
 : NUMBER OF SEQUENCES: 17 :
 : CORRESPONDENCE ADDRESS: :
 : ADDRESS: BIRCH, STEWART, KOLASCH & BIRCH :
 : STREET: 8110 Gatehouse Road, Suite 500 East :
 : CITY: Falls Church :
 : STATE: Virginia :
 : COUNTRY: U.S.A. :
 : ZIP: 2046 :

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025:583
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/351.413
FILING DATE:
APPLICATION NUMBER: US 07/899,072
FILING DATE: 12-JUN-1992

ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-102PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345

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ID# : 246345
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
    LENGTH: 5620 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: double
    TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: plasmid pVEI08 (replicable in E.coli)
FEATURE:
NAME/KEY: -

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NAME/KEY: -

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OTHER INFORMATION: polyadenylation site derived from the napaline
OTHER INFORMATION: synthase gene from Agrobacterium T-DNA"
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US-09-025-583-3

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Query Match 21.7%; Score 1270.4; DB 2; Length 5620;
Best Local Similarity 98.9%; Pred. No. 3e-268;
Matches 1291; Conservative 0; Mismatches 11; Indels 4; Gaps 1;

Qy	2612	tttcgaccgcggtaccocgcgaattcagctcgcgtaccgcgggaattctccgctctagtaaac	2671
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RESULT 7

US-08-064-121-3/c

; Sequence 3, Application US/08064121

; Patent No. 5641664

GENERAL INFORMATION:
APPLICANT: D'HALLUIN, Kathleen
TITLE OF INVENTION: PROCESS FOR TRANSFORMING MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/064.121
FILING DATE: 24-MAY-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90403332.1
FILING DATE: 23-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91401888.2
FILING DATE: 08-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1287 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: fragment of pTTM8
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NAME/KEY: -
LOCATION: 546..881 /label= barnase
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OTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylation site derived from Agrobacterium T-DNA nopaline synthase gene "
US-08-064-121-3
Query Match 21.6%; Score 1269; DB 1; Length 1287;
Best Local Similarity 99.7%; Pred. No. 3.1e-268;
Matches 1283; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
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RESULT 8
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 ; Sequence 3, Application US/08478015
 ; Patent No. 5712135
 ; GENERAL INFORMATION:
 ; APPLICANT: D'HALLUIN, Kathleen
 ; APPLICANT: Gobel, Elke
 ; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
 ; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Burns, Doane, Swecker & Mathis
 ; STREET: P.O. Box 1404
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: United States
 ; ZIP: 22313-1404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/478,015
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 90403332.1
 ; FILING DATE: 23-NOV-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 91401888.2
 ; FILING DATE: 08-JUL-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/064,121
 ; FILING DATE: 23-JUN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McGowan, Malcolm K.
 ; REGISTRATION NUMBER: 39,300
 ; REFERENCE/DOCKET NUMBER: 010830-088
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 836-6620
 ; TELEFAX: (703) 836-2021
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1287 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: fragment of pTtM8
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 ; NAME/KEY: -
 ; LOCATION: 1..545
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 ; OTHER INFORMATION: /note= "Promoter from the TA29 gene of Nicotiana tabacum"
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LOCATION: 546..881 /note= "coding sequence of barnase gene"
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OTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylation
OTHER INFORMATION: site derived from Agrobacterium T-DNA nopaline synthase gene
US-08-478-015-3

Query Match 21.6%; Score 1269; DB 1; Length 1287;
Best Local Similarity 99.7%; Pred. No. 3.1e-268;
Matches 1283; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

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Qy 2691 ataattcatctagttgcgcgtatattttttctatcgctattaaatgtataatt 2750
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Qy 3227 gqcgagctctgaaggttccctttgatgccaccagcgaggtctgtgcttctgaatt 3286
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Qy 3347 acgtgttgataacccggtaccatgagcgaatttcttaagtaaaaaactttgattgagt 3406
Db 567 ACGTGTTGATAAACCGGTACCATTGTTAGTAAATTTCTTTAAGTAAAAAATTTTGGATT 508
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Qy 3467 aacaactgcaaaactaacttttgttggagcatttcagagaaaaatggggagtagcaggct 3526
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Qy 3587 agaaaaagtagcaaaaaattttgtctccacctgatttcagtttatgaaattacattatgaa 3646
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Qy 3887 aaattatccgattatacttagtagat 3913
Db 27 AAATATCCAGTTATACTTAGCTAGAT 1

RESULT 9
US-08-475-975-3/C
; Sequence 3, Application US/08475975
; Patent No. 6002070
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,975
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,121
; FILING DATE: 24-MAY-1993
; APPLICATION NUMBER: EP 90403332.1
; FILING DATE: 23-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620

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; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1287 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: fragment of pTTH8
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..545
; OTHER INFORMATION: /label= PTA29
; OTHER INFORMATION: /note= "Promoter from the TA29 gene of Nicotiana
; OTHER INFORMATION: tabacum"
; FEATURE:
; NAME/KEY: -
; LOCATION: 546..881
; OTHER INFORMATION: /label= barnase
; OTHER INFORMATION: /note= "coding sequence of barnase gene"
; FEATURE:
; NAME/KEY: -
; LOCATION: 882..1287
; OTHER INFORMATION: /label= 3'nos
; OTHER INFORMATION: /note= "3' regulatory sequence containing the
; OTHER INFORMATION: polyadenylation site derived from Agrobacterium
; OTHER INFORMATION: T-DNA nopaline synthase gene "
; US-08-475-975-3

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Matches 1283; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

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QY 2931 ag----ccggaaagtgaattgaccgcgatcagagtttgaagaaaaatttattacacacttt 2986
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QY 3107 ggtcgaattctgaagcctgtagtatagtaataatccgcttcacgcgcgcgcgcgcgcgcgcgc 3166
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QY 3287 ttgtaatgaattatcaggttagcttatgatgtctgaagataatccgcaaccgcgcgcgcgc 3346
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QY 3347 acgtgttgataaacgcgtaccatggttagctaatcttcttaagtaaaaaactttgattgagt 3406
DB 567 ACGTGTGTAACCGGTACCATGGTAGCTAATTTCTTTAAGTAAAAAATTTGATTGAGT 508

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RESULT 10
US-09-084-889-3/C
; Sequence 3, Application US/09084889
; Patent No. 6074877
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/084,889
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,121
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91401888.2
FILING DATE: 08-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1287 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: fragment of pTTW8
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NAME/KEY: -
LOCATION: 1..545
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FEATURE:
NAME/KEY: -
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FEATURE:
NAME/KEY: -
LOCATION: 882..1287
OTHER INFORMATION: /label= 3'nos
OTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylation site derived from Agrobacterium T-DNA nopaline synthase gene "
US-09-084-889-3

Query Match 21.6%; Score 1269; DB 3; Length 1287;
Best Local Similarity 99.7%; Pred. No. 3.1e-268;
Matches 1283; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
Qy 2631 aattcgagctcggtacccgggagcttcctccgagctagtaacatagatgacacccgcgcg 2690
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Db 507 GATGATGTTGTACTGTTTACACTTGCACCAAGGGCATATATAGAGCAACAAGACATACAC 448
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Db 447 AACAACTTGCAAAACTAACTTTTGTGGAGCATTTTCAGAGAAATGGGGAGTAGCAGGCT 388
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Db 207 AGCTTGATTCAAAACTGATTTAATTTACATTTGCTAAATGTGCATCTTCGAGCCTATGT 148
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Db 147 GCGTTTAATTCGAGTAGGATGATATATTAGTACATAAAAAAATCATGTTTGAATCATCTT 88
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Qy 3887 aaattatccagttactacttagctagat 3913
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Db 27 AAATTATCCAGTTTACTTAGCTAGAT 1

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; Sequence 2, Application US/08817188
; Patent No. 6074876
; GENERAL INFORMATION:
; APPLICANT: DE BLOCK, MARC
; TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
; FILE REFERENCE: 2121-0127P
; CURRENT APPLICATION NUMBER: US/08/817,188
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: PCT/EP96/03366
; EARLIER FILING DATE: 1996-07-31
; EARLIER APPLICATION NUMBER: EP 95401844.6
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6548
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pTS172
; NAME/KEY: misc_feature
; LOCATION: Complement((2019)..(2288))
; OTHER INFORMATION: 3' nos: 3' untranslated region containing the
; OTHER INFORMATION: polyadenylation signal of the nopaline synthase
; OTHER INFORMATION: gene of Agrobacterium T-DNA.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((2289)..(2624))
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((2625)..(4313))
; OTHER INFORMATION: PEI: promoter region of E1 gene of rice
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4336)..(5170)
; OTHER INFORMATION: P35S: 35S promoter region of Cauliflower Mosaic
; OTHER INFORMATION: Virus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((5711)..(6262))
; OTHER INFORMATION: bar: region coding for phosphinotricin
; OTHER INFORMATION: acetyltransferase
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6263)..(6496)
; OTHER INFORMATION: 3'g: 3' untranslated region containing the
; OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
; OTHER INFORMATION: T-DNA
; US-08-817-188-2

Query Match          14.2%; Score 832.8; DB 3; Length 6548;
Best Local Similarity 99.8%; Pred. NO. 1.4e-172;
Matches 834; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 234 attgcgtagatgaagagctgagtcgatatattgtgtaatacataaaattgatgatag 293
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QY 294 ctagcttagctcatcgggggatcctagaacgctgtagtctcagatctcgttgacgggcagg 353
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QY 354 accggaagggcggtaccgagcggtgaagtccagctgcccagaaacacacgctcatgcag 413
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QY 414 ttcccgctgttgaagccgcccgcgcagcatgccgcgaggggggcataatccagagcgcctcg 473
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QY 474 tgcagtcgacgctcggttgcgttgggcagcccagatgacagcagccacgctcttgaagccc 533
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QY 774 cgaaagtacacgctgttctctctctctctctctctctctctctctctctctctctct 833
Db 5820 CGAAAGTTGACCGTGTCTCTCGATGTAGTGTGTACAGTGTGTACAGATGTCAGACCCCGCATG 5761

QY 834 tcgcctcgttgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacg 889
Db 5760 TCGCGCTCGTGGCAGCGCGGATGTCGGCGCGGCGTCTGCGGTCTCCATGCTTAT 5705
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RESULT 12

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US-08-894-440-1/c
; Sequence 1, Application US/08894440
; Patent No. 6025546
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Method to obtain male sterile plants
; FILE REFERENCE: NMSCOR
; CURRENT APPLICATION NUMBER: US/08/894,440
; CURRENT FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6548
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pTS174
; NAME/KEY: misc_feature
; LOCATION: (1)..(2003)
; OTHER INFORMATION: pUC19 derived vector sequences (vector)
; NAME/KEY: misc_feature
; LOCATION: Complement((2019)..(2283))
; OTHER INFORMATION: 3' nos: region containing polyadenylation signal
; OTHER INFORMATION: of nopaline synthase gene of Agrobacterium
; NAME/KEY: misc_feature
; LOCATION: Complement((2284)..(2624))
; OTHER INFORMATION: region coding for barnase of Bacillus
; OTHER INFORMATION: amyloliquefaciens
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((2625)..(4313))
; OTHER INFORMATION: promoter of the stamen-specific E1 gene of rice
; OTHER INFORMATION: (PE1)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4336)..(5710)
; OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus (P35S)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5711)..(6262)
; OTHER INFORMATION: region coding for phosphinothricin acetyl
; OTHER INFORMATION: transferase (bar)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6263)..(6496)
; OTHER INFORMATION: region containing polyadenylation signal fo gene 7
; OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
US-08-894-440-1

Query Match          14.2%; Score 831.2; DB 3; Length 6548;
Best Local Similarity 99.6%; Pred. No. 3.1e-172;
Matches 833; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 54 gtacatggtcgataaagaaaggcaattgttagatggttaattcccatcttgaagaaatat 113
Db 6540 GTACATGGTCGATAAGAAAGGCAATTGTTAGATGTTAAATCCCATCTTGAAGAAATAT 6481

QY 414 agtttaaatattattgataaaataacaagtcagggtattatagtcceagcaaaacataa 173
Db 6480 AGTTTAAATATTTATTGATAAAATAACAAGTCAGGTATTATTAGTCCAAAGCAAAACATAA 6421

QY 174 atttattgatgcaagttaaattcagaataatttcataactaactaattatcacgtgctac 233
Db 6420 ATTTATTGATGCAAGTTTAATTTCAGAAATATTTCATAACTGATTATATCAGCTGTGATC 6361

QY 234 attgcgttagatgaagactgagtcgcatattatgtgtaatacatataaattgatgatag 293
Db 6360 ATTCGCCGTAGATGAAGACTGAGTCGCATATTATGTGTAATACATAAAATTGATGATATAG 6301

QY 294 ctagcttagctatcgggggatcctagaacgctgtagctcagatctcgttgagcggcgagg 353
Db 6300 CTAGCTTAGCTATCGGGGGATCCTAGAACCGCTGTCTCAGATCTCGGTGACGGCGAGG 6241

QY 354 accgagcggggtgacccgagcgtgaagtcagctgcccagacagcaaaaccacgtcatgccag 413
Db 6240 ACCGAGCGGGGGGTACCGCGCAGGCTGAAGTCCAGCTGCCAGAAACCCACGTCATGCCAG 6181

QY 414 ttccctgtctgaagccgcccgcgcagcatgcgcggggggcattatccgagcgcctcg 473
Db 6180 TTCCCGTGTGTTGAAGCGGGCCGCCGAGCATGCCGGGGGGCATATCCGAGCGCCTCG 6121

QY 474 tgatgcgcacgctcgggtcgttggcagcccgatgacagcaccacgctcttgaagccc 533
Db 6120 TGATGCGCACGCTCGGGTGTGTTGGCAGCCCGCATGATGACGACGACGCTCTTTGAAGCCC 6061

QY 534 tgtgcctccagggacttcagcaggtgggtgtagagcgtgagccagtcctcgcgtcgtcg 593
Db 6060 TGTGCCTCCAGGAGACTTCACAGGTGGGTGTAGAGCGTGAGAGCCAGTCCCGTCCGCTGG 6001

QY 594 tggcggggggagacgtacacaggtcgactcgcgcgtccagtcgtagggcgttgcgtgcttc 653
Db 6000 TGCGGGGGGAGAGCGTACACGGTCGACTCGCGCGCTCCAGTCGTAGGCGTTGCGTGCCTTC 5941

QY 654 caggggcccgctaggtgagatgcgggagacctcgcgcgtccacacctggcgagcagcaggga 713
Db 5940 CAGGGGCCCGGTAGGCGATCCGGGCGACCTCGCGCGTCCACCTCGCGGAGGAGCGAGGGA 5881

QY 714 tagcgtcccgagcagcagcaggtgctgctccgtccactccctgcggttccgtcggctcgta 773
Db 5880 TAGCGCTCCCGCAGCAGGAGGAGGTGCTGCTCCGTCCACTCTTCCGCTGCGGCTCGGTA 5821
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QY 774 cggaaattgaccgtgttctctcgatgtagtggttgacgatggtgacgacccgcggcatg 833
Db 5820 CGGAAGTTGACCGTGTGCTCGATCTAGTGGTTGACGATGGTGACACCGCGCGCATG 5761

QY 834 tcgcctcgggtgacacggcgagatgctggccggcgctcgtctctgggtccattgttct 889
Db 5760 TCCGCTCGGGTGGCAGCGCGGATGTCGGCGGGCGTCTGCTGGGTCCATGGTTAT 5705

RESULT 13
US-08-894-440-3
; Sequence 3, Application US/08894440
; Patent No. 6025546
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Method to obtain male sterile plants
; FILE REFERENCE: WNSCOR
; CURRENT APPLICATION NUMBER: US/08/894,440
; CURRENT FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 3658
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EcoRI-HindIII
; OTHER INFORMATION: fragment of pVE136
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(26)
; OTHER INFORMATION: polylinker of pUC19
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((28)..(403))
; OTHER INFORMATION: region containing polyadenylation signal of
; OTHER INFORMATION: napaline synthase gene of Agrobacterium T-DNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((404)..(739))
; OTHER INFORMATION: region coding for barnase of Bacillus
; OTHER INFORMATION: amyloliquefaciens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((740)..(1918))
; OTHER INFORMATION: promoter of CA55 gene of Zea mays (PCA55)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1956)..(2788)
; OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus (35S)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2789)..(3340)
; OTHER INFORMATION: region coding for phosphinothricin acetyl
; OTHER INFORMATION: transferase (bar)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3341)..(3623)
; OTHER INFORMATION: region containing polyadenylation signal of
; OTHER INFORMATION: napaline synthase gene of Agrobacterium T-DNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3624)..(3658)
; OTHER INFORMATION: polylinker of pUC19
US-08-894-440-3
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Query Match 12.6%; Score 741.8; DB 3; Length 3658;
Best Local Similarity 99.7%; Pred. No. 8.2e-153;
Matches 743; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


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QY 2630 gaattcagctcgttaccggggatcttcccgatctagtaacatagatgacacccgcgc 2689
D 1 gaattcagctcgttaccggggatcttcccgatctagtaacatagatgacacccgcgc 60
QY 2690 gataattatctcgttgcgcgcctatatttggttctatcgcgtattaaatgtataat 2749
D 61 gataattatctcgttgcgcgcctatatttggttctatcgcgtattaaatgtataat 120
QY 2750 tgcgggactcctaataaaccacccatctcacaataacgctcgcgtatcattatgtataat 2809
D 121 tgcgggactcctaataaaccacccatctcacaataacgctcgcgtatcattatgtataat 180
QY 2810 attacatgcttaacgtaattcaacagaaattatgataatcgcgaagccgcgcaaca 2869
D 181 attacatgcttaacgtaattcaacagaaattatgataatcgcgaagccgcgcaaca 240
QY 2870 gattcaactcctaagaacttatttgcgaatgtttggaacgatcgtcgtcgatcctccta 2929
D 241 gattcaactcctaagaacttatttgcgaatgtttggaacgatcgtcgtcgatcctccta 300
QY 2930 gagccggaagtgaattgacgcagatgattgaaagaaattattacacatttatg 2989
D 301 gagccggaagtgaattgacgcagatgattgaaagaaattattacacatttatg 360
QY 2990 taaagctgaaaaaacgctcccgaggagccggttttttcgttatctgattttgttaa 3049
D 361 taaagctgaaaaaacgctcccgaggagccggttttttcgttatctgattttgttaa 420
QY 3050 aggtctgataatggtccgttttttgaataacagcagtcgctgagtaagaatccggt 3109
D 421 aggtctgataatggtccgttttttgaataacagcagtcgctgagtaagaatccggt 480
QY 3110 ctgaattctgaagcctgagtgatagtaataatccgcttcacgcagcttgcgtcgcgttt 3169
D 481 ctgaattctgaagcctgagtgatagtaataatccgcttcacgcagcttgcgtcgcgttt 540
QY 3170 tgcgcggagtttgcctccctcttgaagagatgctccgcgagcttcttcccgag 3229
D 541 tgcgcggagtttgcctccctcttgaagagatgctccgcgagcttcttcccgag 600
QY 3230 cgaagctgaaggtcccttttgatgccaccacgcgaggggttgcgttcgtatttg 3289
D 601 cgaagctgaaggtcccttttgatgccaccacgcgaggggttgcgttcgtatttg 660
QY 3290 taatgaattatcaggtagcttatgatctgagataatccgcaaccccgatcaaacg 3349
D 661 taatgaattatcaggtagcttatgatctgagataatccgcaaccccgatcaaacg 720
QY 3350 tgttgataacccggtaccatggtagc 3374
D 721 tgttgataacccggtaccatggtcgc 745
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RESULT 14

US-08-351-413-17

; Sequence 17, Application US/08351413

; Patent No. 5750867

; GENERAL INFORMATION:

; APPLICANT: Williams, Mark

; APPLICANT: Leemans, Jan

; TITLE OF INVENTION: Maintenance of male-sterile plants

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESSES:

; ADDRESSES: BIRCH, STEWART, KOLASCH & BIRCH

; STREET: 8110 Gatehouse Road, Suite 500 East

; CITY: Falls Church

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 2046

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/351,413
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/899,072
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/970,849
; FILING DATE: 03-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 2121-102PCT
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4808 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: EcoRI-HindIII fragment of plasmid pTS218
; FEATURE:
; NAME/KEY:
; LOCATION: complement (18..401)
; OTHER INFORMATION: /label= 3'nos
; OTHER INFORMATION: /note= "3' regulatory sequence containing the
; OTHER INFORMATION: polyadenylation site derived from Agrobacterium
; OTHER INFORMATION: T-DNA nopaline synthase gene"
; FEATURE:
; NAME/KEY:
; LOCATION: complement (402..737)
; OTHER INFORMATION: /label= barnase
; OTHER INFORMATION: /note= "coding region of the barnase gene of
; OTHER INFORMATION: Bacillus amyloliquefaciens"
; FEATURE:
; NAME/KEY:
; LOCATION: complement (738..1944)
; OTHER INFORMATION: /label= PZM13
; OTHER INFORMATION: /note= "promoter region of the Zm13 gene of Zea
; OTHER INFORMATION: mays"
; FEATURE:
; NAME/KEY:
; LOCATION: complement (1945..2281)
; OTHER INFORMATION: /label= 3'nos
; FEATURE:
; NAME/KEY:
; LOCATION: complement (2282..2554)
; OTHER INFORMATION: /label= barstar
; OTHER INFORMATION: /note= "coding region of the barstar gene of
; OTHER INFORMATION: Bacillus amyloliquefaciens"
; FEATURE:
; NAME/KEY:
; LOCATION: complement (2555..3099)
; OTHER INFORMATION: /label= PTA29
; OTHER INFORMATION: /note= "promoter region of the TA29 gene of
; OTHER INFORMATION: Nicotiana tabacum"
; FEATURE:
; NAME/KEY:
; LOCATION: 3100...3932
; OTHER INFORMATION: /label= 35S3
; OTHER INFORMATION: /note= "35S3" promoter sequence derived from
; OTHER INFORMATION: cauliflower mosaic virus isolate CabBB-J1"
; FEATURE:
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: NAME/KEY: -
: LOCATION: 3933...4484
: OTHER INFORMATION: /label= bar
: OTHER INFORMATION: /note= "coding region of the phosphinothricin
: OTHER INFORMATION: acetyltransferase gene"
: FEATURE:
: NAME/KEY: -
: LOCATION: 4485...4763
: OTHER INFORMATION: /label= 3' nos
: FEATURE:
: NAME/KEY: -
: LOCATION: 2333...2356
: OTHER INFORMATION: /label= BXOL2
: OTHER INFORMATION: /note= "region corresponding to oligonucleotide
: OTHER INFORMATION: BXOL2"
: FEATURE:
: NAME/KEY: -
: LOCATION: complement (2538..2586)
: OTHER INFORMATION: /label= TA29SBXOL2
: OTHER INFORMATION: /note= "region complementary to oligonucleotide
: OTHER INFORMATION: TA29SBXOL2"
: FEATURE:
: NAME/KEY: -
: LOCATION: complement (2800..2823)
: OTHER INFORMATION: /label= PTA29OL5
: OTHER INFORMATION: /note= "region complementary to part of
: OTHER INFORMATION: oligonucleotide PTA29OL5"
: US-08-351-413-17

Query Match          12.4%; Score 729.4; DB 1; Length 4808;
Best Local Similarity 99.3%; Pred. No. 4.8e-150;
Matches 744; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

Qy 2630 gaattcagctcggtaccggggatctcccgatctagtaacatagatgacaccgcgcg 2689
Db 1 GAATTCGAGCTCGTACCCGGGGATCTCCCGATCTAGTAACATAGATGACACCGCGCGC 60

Qy 2690 gataattatctagtgtgcgcgtatatattgttttctatcgcgattaaatgataat 2749
Db 61 GATAATTATCTAGTTGCGCGGTATATTGTTTCTATCGGTATTAATGTATAAT 120

Qy 2750 tgcgggactctaatataaaacccatctcataataaacgctcatgcatatttaatt 2809
Db 121 TCGGGGACTCTAAATCAATAAAACCCATCTCATATAATACGTCATGCATTTACATTAAT 180

Qy 2810 attacatgcttaacgtaattcaacagaaattatgataatcatcgaaaccgcgcaaca 2869
Db 181 ATTACATGCTTAACGTAATTCAACAGAAATTTATGATAATCATCGCAAGACCGCAACA 240

Qy 2870 ggattcaatcttaagaaccttattgcaaatgtttgaacgatctgctcgatctctcta 2929
Db 241 GGATTCAATCTTAAGAAACTTTATTGCAAAATTTTGAACGATCTGCTTCGGATCCTCTA 300

Qy 2930 gag----ccggaaagtgaattgaccgatcagagatttgaagaaaaattattacacatt 2985
Db 301 GAGNNNCCGGAAAGTGAATTTGACCATCAGAGTTTGAAGAAAAATTTATTACACACTT 360

Qy 2986 tatgtaagctgaaaaaacgctccgcaggaagcggttttttctgtatctgattttt 3045
Db 361 TATGTAAGCTGAAAAAANACGGCCCTCCGCAGGAAGCGGTTTTTTTCGTATCTGATTTT 420

Qy 3046 gtaaggtctgataatggtcgtgtttgttataatcagccagtcgctgagtaagaatc 3105
Db 421 GTAAAGCTTGATAATGTCGCTGTTGTTTGTAAATACGCCAGTCGCTTGAGTAAAGAAATC 480

Qy 3106 cggctgaattctgaagcctgatgtagtataatccgcttcaacgccattgttcgtccg 3165
Db 481 CGGTCTGAATTTCTGAAGCCTGATGTATAGTTAATATCCCGTTTACGCCCATGTTTCGTCGG 540

Qy 3166 cttttcccgaggattgcttccctcttggagagatgctccgcagatgcttttccccc 3225
Db 541 CTTTTCGCGGGAGTTTGGCCTTCCCTGTTTGAGAAGATGTCCTCCGCGGATGCTTTTCCCC 600
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Qy 3226 ggagcgacgtctgcaaggtttcccttttgatgccaccacgacgaggggttgcgtctgat 3285
Db 601 GGAGCGACGCTGCGAAGGTTCCCTTTTGTATGCCACCGAGCGAGGCTTGTGCTTCTGAT 660

Qy 3286 ttgtaatgtaattatcaggttagcttatgtatgtatctgaagataatccgcaaccccgatca 3345
Db 561 TTTGTAATGTAATTATCAGGTAGCTTATGATATGCTGTAAGATATCCGCAACCCCGTCA 720

Qy 3346 aacgtgttgataaccggtaccatggtagc 3374
Db 721 AACGTGTTGATAACCGGTACCATGGTTGC 749

RESULT 15
US-09-583-17
: Sequence 17, Application US/09025583
: Patent No. 5977433
: GENERAL INFORMATION:
: APPLICANT: Williams, Mark
: APPLICANT: Leemans, Jan
: TITLE OF INVENTION: Maintenance of male-sterile plants
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
: STREET: 8110 Gatehouse Road, Suite 500 East
: CITY: Falls Church
: STATE: Virginia
: COUNTRY: U.S.A.
: ZIP: 2046
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/025,583
: FILING DATE:
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/351,413
: FILING DATE:
: APPLICATION NUMBER: US 07/899,072
: FILING DATE: 12-JUN-1992
: PRIOR APPLICATION NUMBER:
: APPLICATION NUMBER: US 07/970,849
: FILING DATE: 03-NOV-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Svensson, Leonard R.
: REGISTRATION NUMBER: 30,330
: REFERENCE/DOCKET NUMBER: 2121-102PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 205-8000
: TELEFAX: (703) 205-8050
: TELEX: 248345
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4808 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: EcoRI-HindIII fragment of plasmid pTS218
: FEATURE:
: NAME/KEY: -
: LOCATION: complement (18..401)
: OTHER INFORMATION: /label= 3' nos
: OTHER INFORMATION: /note= "3' regulatory sequence containing the
: OTHER INFORMATION: polyadenylation site derived from Agrobacterium
: OTHER INFORMATION: T-DNA nopaline synthase gene"
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FEATURE:
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LOCATION: complement (402..737)
OTHER INFORMATION: /label= barnase
OTHER INFORMATION: /note= "coding region of the barnase gene of
OTHER INFORMATION: Bacillus amyloliquefaciens"
FEATURE:
NAME/KEY: -
LOCATION: complement (738..1944)
OTHER INFORMATION: /label= PZM13
OTHER INFORMATION: /note= "promoter region of the Zml3 gene of Zea
OTHER INFORMATION: mays"
FEATURE:
NAME/KEY: -
LOCATION: complement (1945..2281)
OTHER INFORMATION: /label= 3'nos
FEATURE:
NAME/KEY: -
LOCATION: complement (2282..2554)
OTHER INFORMATION: /label= barstar
OTHER INFORMATION: /note= "coding region of the barstar gene of
OTHER INFORMATION: Bacillus amyloliquefaciens"
FEATURE:
NAME/KEY: -
LOCATION: complement (2555..3099)
OTHER INFORMATION: /label= PTA29
OTHER INFORMATION: /note= "promoter region of the TA29 gene of
OTHER INFORMATION: Nicotiana tabacum"
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NAME/KEY: -
LOCATION: 3100..3932
OTHER INFORMATION: /label= 3S53
OTHER INFORMATION: /note= "3S53 promoter sequence derived from
OTHER INFORMATION: cauliflower mosaic virus isolate CabBB-JI"
FEATURE:
NAME/KEY: -
LOCATION: 3933..4484
OTHER INFORMATION: /label= bar
OTHER INFORMATION: /note= "coding region of the phosphinothricin
OTHER INFORMATION: acetyltransferase gene"
FEATURE:
NAME/KEY: -
LOCATION: 4485..4763
OTHER INFORMATION: /label= 3'nos
FEATURE:
NAME/KEY: -
LOCATION: 2333..2356
OTHER INFORMATION: /label= BXOL2
OTHER INFORMATION: /note= "region corresponding to oligonucleotide
OTHER INFORMATION: BXOL2"
FEATURE:
NAME/KEY: -
LOCATION: complement (2538..2586)
OTHER INFORMATION: /label= TA29SBXOL2
OTHER INFORMATION: /note= "region complementary to oligonucleotide
OTHER INFORMATION: TA29SBXOL2"
FEATURE:
NAME/KEY: -
LOCATION: complement (2800..2823)
OTHER INFORMATION: /label= PTA29OL5
OTHER INFORMATION: /note= "region complementary to part of
OTHER INFORMATION: oligonucleotide PTA29OL5"
IS-09-025-583-17
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Best Local Similarity	99.3%	Pred. No. 4.8e-150;		
Matches 744;	Conservative	0;	Mismatches 1;	Indels 4;
			Gaps	1;

Qy	2630	gaattcggagctcggtaccCGGGgatatcttcccgatcttagtaacatagatacacacgcgcg 	2689
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Job time: 14717 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 - 2: gb_est2:*
 - 3: gb_est3:*
 - 4: gb_est4:*
 - 5: gb_est5:*
 - 6: gb_est6:*
 - 7: gb_est7:*
 - 8: gb_est8:*
 - 9: gb_est9:*
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- 44: em_esthum10:*
- 45: em_esthum11:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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QY	1684	taaacaaagtccaaaaaaactctcgaagtctccattt	1722
Db	732	CAATTCCAAAAAAACTCCCAATTCCTCATCTCCCTTTT	770
RESULT	2		
LOCUS	AQ250179	820 bp DNA	GSS
DEFINITION	T24K7-T7.1 TAMU Arabidopsis thaliana genomic clone T24K7,		DNA
ACCESSION	AQ250179	sequence.	
VERSION	AQ250179		
KEYWORDS	AQ250179.1	GI:3700262	
SOURCE	GSS.		
ORGANISM	thale cress.		
	Arabidopsis thaliana		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.		
REFERENCE	1 (bases 1 to 820)		
AUTHORS	Feng,J., Dewar,K., Buehler,E., Kim,C., Li,Y., Shinn,P., Sun,H. and Ecker,J.		
TITLE	BAC End Sequences at ATCC		
JOURNAL	Unpublished (1997)		
COMMENT	Contact: Ecker J.		
	Arabidopsis Thaliana Genome Center		
	University of Pennsylvania		
	Dept. of Biology, University of Pennsylvania, Philadelphia, PA 19104		
	Tel.: 215-898-9384		
	Fax: 215-898-8780		
	Email: jecker@atgenome.bio.upenn.edu		
	Seq primer: T7		
	Class: BAC ends.		
FEATURES	Location/Qualifiers		
source	1..820		
	/organism="Arabidopsis thaliana"		
	/strain="Columbia"		
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	/note="Vector: BeloBACII; Site_1: HindIII; Site_2: HindIII"		
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BASE COUNT	257 a 149 C 140 G 272 T		
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Query Match	9.4%; Score 554.2; DB 226; Length 820;		
Best Local Similarity	87.8%; Pred. No. 5.1e-100;		
Matches	685; Conservative 0; Mismatches 84; Indels 11; Gaps 7;		
QY	968	ctttgagtgatcgagaggtctagatacatagagatgaagtgcattgacacg	1027
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QY	1028	tbgatttttgagtgaggatgtgagggttaatttacttggtaacgcccacaaagcc	1087
Db	102	TTGGATTTTGAGTGTGGATATGTGTGAGGTTAATTTACTTGGTACGGCCAAAGGCC	161
QY	1088	taagagaggtgttgagacccttcaggttgacgcgtgggaataatgccagtggaaga	1147
Db	162	TAAAGAGATGTGTGAGACCCCTTATCGCTTTGAACCGCTGGAATATGCCACGTGAAGA	221
QY	1148	taattccatgaattcttcgttacttatgagtgaaattgtgtgagtgagtgagtgctt	1207
Db	222	TAAATCCATGAATCTTATCGTTATCATGAGTGAAATTCGTGATGGTGGAGTGTGCTT	281
QY	1208	gctcatttacttgcctgggtggacttggcccttccttatgggggaatttatatttactt	1267

BASE COUNT ORIGIN	203 a	79 c	60 g	232 t	5 others
Query Match	5.4%; Score 315.6; DB 226; Length 579;				
Best Local Similarity	78.7%; Pred. No. 1.4e-52;				
Matches 440; Conservative	0; Mismatches 104; Indels 15; Gaps 5;				
QY 1129	aataatgccacgtggaagataattccatgaattcttcgttatctctatctatgagtgaaattgtg 1188				
Db 1	AATAAATGNANGTGAATAATAATCCATGAATCTTATCGTTATCTATGAGTTGAAATGTG 60				
QY 1189	tgatggtgagtggtgcttgcctcatcttttacttctgcctggtggaacttggcccttctctatg 1248				
Db 61	TGATGTGGAGTGTGCTCTCTCATTTTACTTTTCTGGTGGAAATTTGCCCTTTCTCTTATG 120				
QY 1249	gggaatttatatttacttactagagctttcatacccttttttacccttgattttagt 1308				
Db 121	GGAAATTTATATNTTACTTACTATAGAGCTTTTCATCACCTTTTNTTAACTTGGATTTATT 180				
QY 1309	taatatataatggtgatgtatcatgaataaaaaatgggaaaatttttgaatttgcactgctaa 1368				
Db 181	TTATATTTAATGCTATCAATCATGAATAAANAATGGGAAA-TTTTGAATTTGTACTGCTAA 239				
QY 1369	atgcataagattggtggaactgtggaatatatatatttttcttcaatttaaaagcaaaatttg 1428				
Db 240	ATGCATAAAATTAGGTGAAACTGTGGAATATATATTTTTTTCATTTTAAAGCAAAATTTG 299				
QY 1429	cctttactagaattacaatatagaaaaatatataacattcaaaataaaaaatgaaaaataa 1488				
Db 300	CCTTTTACTAAAATTTTAAATTTAGAAAAAT-TTTTACATTTCCAAATTTAAATGAAATAA 358				
QY 1489	gaactttcaaaaacagaaactatgtttaatgtgtaaagattagtcgcacatcaagtcatc 1548				
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QY 1549	tgtacaatatgttacacaagtcataagaagcccaaaagtagcacgtctcaataaaacta 1608				
Db 410	TTTTTTTAAAAAATTTTAAAAAATTTTAAACCCCAAAAATTTTCCTTCTCAATAAATTAA 469				
QY 1609	aaggtccacgaaatattacaatcaatcaagcccaacaaagttattgatcaaaaaaaaaa 1668				
Db 470	AA----TTCCGAAAAATTTTCAATCTTTTACCCCAAAAATTTTATTTTATTCAAAAAANA 525				
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RESULT 4					
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LOCUS	T24K7-T7 TAMU Arabidopsis thaliana genomic clone T24K7, DNA				
DEFINITION	sequence.				
ACCESSION	AQ249824				
VERSION	AQ249824.1 GI:3699907				
KEYWORDS	GSS.				
SOURCE	thale cress.				
ORGANISM	Arabidopsis thaliana				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 451)				
AUTHORS	Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and Ecker, J.				
TITLE	BAC End Sequences at ATGC				
JOURNAL	Unpublished (1997)				
COMMENT	Contact: Ecker J. Arabidopsis Thaliana Genome Center University of Pennsylvania Dept. of Biology, University of Pennsylvania, Philadelphia, PA 19104 Tel: 215-898-9384				
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source	Location/Qualifiers				
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	/sex="hermaphrodite"				
	/notes="Vector: BelobACII; Site_1: HindIII; Site_2: HindIII				
	; Produced by Rod Wing"				
BASE COUNT	145 a	54 c	64 g	185 t	3 others
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Query Match	5.3%; Score 312.6; DB 226; Length 451;				
Best Local Similarity	84.6%; Pred. No. 5.3e-52;				
Matches 384; Conservative	0; Mismatches 67; Indels 3; Gaps 3;				
QY 1118	tgaacgcctgaataatgccacgtggaagataattccatgaattcttcttctatga 1177				
Db 1	TGAACCCGCTGGAAATAATGCCACGTGGAATATAATTCATGAATCTTATPCGTTATCTATGA 60				
QY 1178	gtgaaattgtgtgatggtggtgagtggtcttgcctcatctttacttgcctggcgaccttgccc 1237				
Db 61	GTGANATGTGTGATGCTGGAGTGTGCTTCTCATTTTACTTGCCTGGTGGACTTGGCC 120				
QY 1238	ctttccttatgggaatttatattttacttacttagacttcttccatccctttttttacc 1297				
Db 121	CTTTCCCTATGGGAATTTATATTTTACTTACTATAAAGTTTTCAAAACCTTTTNTNTAAC 180				
QY 1298	ttggatttacttaataataatggtgatgttcataagataaaaaatggaaaatttttgaatt 1357				
Db 181	TTTGTATTTTTTTTTTATATGTTATGTTATGATCAATCAATAACAATGGGACATCTTGAAT 240				
QY 1358	tgtactgtcaaatgcataagattaggtgaaactgtgaaactatatttttttctatttaa 1417				
Db 241	TGFACTGCTAAATGCAATAAANAATAGTGAAA-TGTGGAATATATA-TTTTTTCATTAAA 298				
QY 1418	agcaaaatttgccttttacttagaattataataatagaaaaatatatacaattcaataaa 1477				
Db 299	AGCAAAATTTGCCCTTTTATTAATAAATTTATTAATTAGAAAAAT-TTTTACTTTCCAATAA 357				
QY 1478	aatgaaaaataagaactttcaaaaaacagaaactatgtttaatgtgtaagaagtaatgcac 1537				
Db 358	ATTGAAAATTAACCTTCTCAAAAACAGAACTATGTTTATTTTATATAAAATTTATCCAA 417				
QY 1538	atcaagtcactgttacaatatgttacaacaagt 1571				
Db 418	TCTAGTTCATCTGTTTAATATATTTTATAACAAT 451				
RESULT 5					
CNS0021J					
LOCUS	1101 bp DNA GSS 03-JUN-1999				
DEFINITION	Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR05N11 of RPCI-98 library from drosophila melanogaster (fruit fly), genomic survey sequence.				
ACCESSION	AL061936				
VERSION	AL061936.1 GI:4940214				
KEYWORDS	GSS.				
SOURCE	fruit fly.				
ORGANISM	Drosophila melanogaster				
REFERENCE	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
AUTHORS	1 (bases 1 to 1101)				
TITLE	Genoscope.				
JOURNAL	Direct Submission				
COMMENT	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :				

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and
 Aaron Mamoser in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPci-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain y2; cn bw sp, the same strain used for the BDGP's
 p1 and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
 FEATURES
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 Matches 346; Conservative 41; Mismatches 479; Indels 0; Gaps 0;
 QY 1254 ttatatattactatagaggtttcattacacotttttttaoactggattgtaata 1313
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 QY 1314 tataatggtatgattcattggaataaattggaattttgaaatttgaattgactgcaatgca 1373
 Db 73 TTTTNNNAANAANAKAATNATAATTTTAAATTAATAAKAKDPAAATAAANAHA 132
 QY 1374 taagattaggtgaactgtggaatatatttttccatttaaaagcaaatgtgcttt 1433
 Db 133 AAAAAGTGTTCATGAAAGTTTAAAAAAAATAAAAAAATAAAAAAANNCTNNNC 192
 QY 1434 tactagattataatagaaaataatacaattcaataaataaataaataaactgaact 1493
 Db 193 NNAANNAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 252
 QY 1494 tcaaaaaacagaaactatgtttatgtgtaagattagtcgcacatcaagtcattcttca 1553
 Db 253 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAA 312
 QY 1554 caatatgtttacaacagtcataagcccaaaagtagtcagcgtcttaataaactaaagag 1613
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 QY 1734 attgaaactatcacacaaacagtcagataaactctctctctggcctgtctccacac 1793
 Db 493 AAAAAAANAANAANAANAATAATTAATTTATTTTNTTNTTNTTNTTNTTNTT 552
 QY 1794 tctacataacttccctacatcggaattgatttttactgtacacttttccgttgcattgat 1853
 Db 553 TTTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTT 612
 QY 1854 attgatagatgtttgtgaaacaaactaatgggttgaacaaatcgaagtcaggaattgatt 1913

Db 613 AWWAAAAAAAWTTTTTAAAWATTTTTTTTTTAAATAATAAAAAAAATATAAAWTT 672
 QY 1914 tgggtccagattttcccgagagcttcttagtagaagcccatccagagaaatttactagta 1973
 Db 673 WTTTATWATWAAATWAAATTTTAAAAWTTTTTTTAAWTTTTTTTAAAAWTTTATTA 732
 QY 1974 aaataaattcccaattgggtttcttattatgtgccaaattcaataattatagagata 2033
 Db 733 WTTTAAAAAATWATWATWTTTAAATTTTTTAAATAATAAAATTTTAAATTA 792
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 Db 793 TTTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTT 852
 QY 2094 ctacgtcagatattccaacttttaaaa 2119
 Db 853 TTTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTT 878
 RESULT 6
 CNS036A2 625 bp DNA GSS 15-MAY-2000
 LOCUS Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
 DEFINITION 215D15 of library G from Tetraodon nigroviridis, genomic survey
 sequence.
 ACCESSION AL229763
 VERSION AL229763.1 GI:7888758
 KEYWORDS GSS; genome survey sequence.
 SOURCE Tetraodon nigroviridis.
 ORGANISM Tetraodon nigroviridis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 Tetraodontidae; Tetraodon.
 REFERENCE 1 (bases 1 to 625)
 AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
 Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
 Weissenbach,J.
 TITLE Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish tetraodon nigroviridis
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 625)
 AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
 Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
 Saurin,W. and Weissenbach,J.
 TITLE Human gene number estimate provided by genome wide analysis using
 Tetraodon nigroviridis DNA sequence
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 625)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
 COMMENT This sequence is a single read and was generated as part of a large
 scale clone-end sequencing project of the Tetraodon nigroviridis
 genome. For more information, please take a look at
<http://www.genoscope.cns.fr/Tetraodon>.
 FEATURES
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 BASE COUNT 394 a 39 c 4 g 170 t 18 others
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 Best Local Similarity 49.0%; Pred. No. 3e-08;
 Matches 226; Conservative 6; Mismatches 231; Indels 0; Gaps 0;

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QY 1299 tggatttagttaataatagtgatcatgaataaaatggggaatttttgaattt 1358
Db 196 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| 255
QY 1359 gtactgctaaatgataagattagggtgaaactgtgggaattattttttttcatttaaa 1418
Db 256 ATAAGATATATATAAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 315
QY 1419 gcaaaatttgccttttctactagaattataaaatagaaaaatataacattcaataaaa 1478
Db 316 TWAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 375
QY 1479 atgaaataagaactttcaaaaacagaactatgtttaaagtgtaaagatttagtcgaca 1538
Db 376 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 435
QY 1539 tcaagtcctctgtttacaaatgtttacaaagtcataagcccaagaagtttagcagctc 1598
Db 436 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 495
QY 1599 aaataaactaaagagtcacgaaatattcaaatatagcccaagaagtttagtc 1658
Db 496 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 555
QY 1659 aaaaaaaagcccaagaagtcataagtcacaaagtcacaaagtcacaaagtcacaaag 1703
Db 556 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600

RESULT 7
CNS00EVL 1101 bp DNA GSS 04-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC:
DEFINITION BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL069706
VERSION AL069706.1 GI:4949849
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL

COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osogawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.
Location/Qualifiers
1..1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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BASE COUNT 419 a 91 c 60 g 299 t 232 others
ORIGIN

Query Match 1.6%; Score 91.4; DB 219; Length 1101;
Best Local Similarity 34.5%; Pred. No. 5.4e-08;
Matches 206; Conservative 100; Mismatches 291; Indels 0; Gaps 0;

QY 4275 ttttttctgctccaaataagtgagtttttttagatttcaaaaatgatttaatttttt 4334
Db 504 WWWWATTTTTWWWWTWTATTTTWWWWTWTATTAATAAATAAATAAATAAATAAATAA 563
QY 4335 ttactacagtcgacctggagtaaatgggtgtgtggagtgatgtgtaaaatgtttatgaa 4394
Db 564 ATTAATAAATTTAAATAAATTAATTAATTAATAAATTTAAATAAATAAATAAATAA 623
QY 4395 gaaatagtaaggttcaatagatcaatttctcatttgaatttgaatttgaatttc 4454
Db 624 WATAAATAATTTTAAATAAATTAATTAATTAATAAATAAATAAATAAATAAATAA 683
QY 4455 ttaactctgtgtgaaacacacacacacacacacacacacacacacacacacacacac 4514
Db 684 WAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 743
QY 4515 atattttggaagcgactaaataaaacttttctcatttatacgaacacctaaacacgca 4574
Db 744 AATWAWATAATATWATAATATATTTTAAWWATWWAWWWTATATAATAAATAAATAA 803
QY 4575 tatggtgagttcttagggaattcaaatcactaaatttaataaaagaagaacaaagtatcaa 4634
Db 804 WATAAATAAWATAWATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 863
QY 4635 tacatatgatttacacgcgtcaaacacacacacacacacacacacacacacacacacac 4694
Db 864 WAATWATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 923
QY 4695 atccaaatagctcccccctataacttaacataaaataaccagcgcaatgtattata 4754
Db 924 AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 983
QY 4755 tgcataatttatattataatctgtataatcatgtataatcaatgtatactatgtata 4814
Db 984 TATWTATATATWWTATWATAATATATTTTAAWWTATATTTTAAWAAATAAATAAATA 1043
QY 4815 tggtagaaaaagtaaacaaattataatagccgctatttggtagaaatcccttaata 4871
Db 1044 WWTWATAATATAWAAWAAATTAATTTATATATATAAATAAATAAATAAATAAATAA 1100

RESULT 8
CNS00EVL/c 1101 bp DNA GSS 04-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC:
DEFINITION BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL069706
VERSION AL069706.1 GI:4949849
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL

COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
- Web : www.genoscope.cns.fr
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
```

The BDGP is constructing a physical map of the *Drosophila melanogaster* genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP *Drosophila melanogaster* BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Peter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial, *ECORI* digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain y2; cn bw, the same strain used for the BDGP's p1 and Est libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source

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Location/Qualifiers
1. .1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_1db="RpCI-98"
/clone_2db="BACR9B23"
/note="end : 77"

419 a 51 c 60 299 t 232 others
BASE COUNT
ORIGIN

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Query Match	1.5%	Score 90.8;	DB 219;	Length 1101;
Best Local Similarity	35.7%	Pred. NO. 7e-08;		
Matched	23%			

[illegible]

RESULT	9
CNS0039G	
LOCUS	
DEFINITION	

LOCUS	CNS00039G	1101 bp	DNA	GSS	03-JUN-1999			
DEFINITION	Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K10 of RPECI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.							
ACCESSION	AL063921							
VERSION	AL063921.1	GI:4941778						
KEYWORDS	GSS.							
SOURCE	fruit fly.							
ORGANISM	Drosophila melanogaster							
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyridioidea; Drosophilidae; Drosophila.							
REFERENCE	1. Theasac, V. et al.							

REFERENCE
AUTHORS
TITLE
JOURNAL

TITLE
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
JP 191 91006 EVRY cedex - FRANCE (E-mail : segréf@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
JOURNAL
COMMENT

COMMENT

determination of this BAC end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RC1-98 and was constructed from partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

[illegible]

```

source
1. 1101
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR08K10"
/note="end : TTT3"

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BASE COUNT
ORIGIN

BASE COUNT	201 a	64 c	131 g	202 t	503 others
ORIGIN					

Query Match

[illegible]

isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES	source	Location/Qualifiers
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		/db_xref="taxon:7227"
		/clone_lib="RPCI-98"
		/clone="BACR14H09"
		/note="end : TET3"
BASE COUNT	404 a 54 c 40 g	251 t 193 others
ORIGIN		
Query Match 1.5%; Score 88.6; DB 219; Length 942;		
Best Local Similarity 40.5%; Pred. No. 1.9e-07;		
Matches 238; Conservative 46; Mismatches 304; Indels 0; Gaps 0;		
QY	1169	tatcatgaggaatgtgtgagggaggtgctgtcatttacttgcctgggtg 1228
DB	311	TWTATATT 370
QY	1229	gacttggcccttcttatggggaatttatatttacttactatagcttcatcactt 1288
DB	371	TTTTTTTTTTTTTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTK 430
QY	1289	tttttacctggatttagttkaataataatggtatgattcatgaataaaatgggaat 1348
DB	431	TTTTTTTKTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 490
QY	1349	tttgaattgtactgctaaatgcataagattagtggaactgtggaatatattttt 1408
DB	491	TNGTKGCTTTTTTTTGGGTGCGGTGGGCGGTGTTTTTTTGTGTTTNG 550
QY	1409	tatttaaaagcaaatgtcctttactagaattataaatatagaaataataacat 1468
DB	551	TGTGTAAPAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAA 610
QY	1469	tcaataaaatgaaataagaactttcaaaaaacagaaactgtttaatgtgaagat 1528
DB	611	AAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAA 670
QY	1529	tagtcgcacatcaagtcattctgttacaatatgttacaagaagtcagccacaagt 1588
DB	671	AAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAA 730
QY	1589	tagcagtcctaaataaactaaagagtcacagaaaatatatacaaatcaagcccaacaa 1648
DB	731	AAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAA 790
QY	1649	gtattgatcaaaaaaaacgcccacaaagctaaacaaagtcacaaaaaaacttct 1708
DB	791	AAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAA 850
QY	1709	caagtctccattctctttagaacattgaaactatacacaaacaa 1756
DB	851	AAAMAMAMCMAMMACMCMCMCMCMCMAMAMAMAMAMAMCMCMCM 898
RESULT 13		
CNS0039C/c		
LOCUS	CNS0039G	1101 bp DNA
DEFINITION	Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.	
ACCESSION	AL063921	
VERSION	AL063921.1	GI:4941778
KEYWORDS	fruit fly.	
SOURCE	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
		03-JUN-1999

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)

Genoscope.

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoeawa and Aaron Mammoss in Piter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

[illegible]

[illegible]

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Query Match      1.5%   Score 85.6;   DB 105;   Length 529;
Best Local Similarity 44.4%;   Pred. No. 7.3e-07;
Matches 213;   Conservative 28;   Mismatches 239;   Indels    0;   Gaps
OY 1287 tttttttacottggattgtaataatataaatgttgatcatcaatgaataaaatggaaa 1346
||||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
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